

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd..

OM protein - protein search, using sw model

Run on: November 8, 2004, 08:05:27 ; Search time 44.8163 Seconds  
(without alignments)  
3132.595 Million cell updates/sec

Title: US-09-830-693B-27  
Perfect score: 1250  
Sequence: 1 SLALSTADQMSVALLDAEP.....CKNVVPLYDLLEMLDAHRL 244

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1239.5	99.2	595	1 ESRI_HUMAN	P03372 homo sapien
2	1205.5	96.4	596	2 Q6Q1S5	Q6Q1S5 bos taurus
3	1205.5	96.4	596	2 AAS46251	AAS46251 bos taurus
4	1204.5	96.4	599	1 ESRI_MOUSE	P19785 mus musculus
5	1200.5	96.0	600	1 ESRI_RAT	P06211 rattus norv
6	1197.5	95.8	595	1 ESRI_PIG	Q29040 sus scrofa
7	1192.5	95.4	595	1 ESRI_MESAU	Q9QZJ5 mesocricetu
8	1179.5	94.4	587	2 Q8UWB0	Q8UWB0 caiman croc
9	1179.5	94.3	594	1 ESRI_HORSE	Q9TV98 equus caball
10	1177.5	94.2	587	1 ESRI_PORGU	Q91250 poephila gu
11	1176.5	94.1	589	1 ESRI_CHICK	P06212 gallus gall
12	1175.5	94.0	587	2 Q765N7	Q765N7 alligator m
13	1175.5	94.0	587	2 BAD08348	BAD08348 alligator
14	1172.5	93.8	589	2 Q8AYH0	Q8AYH0 coturnix co
15	1170.5	93.6	353	2 Q8CCK8	Q8CCK8 cavia porce
16	1164.5	93.2	431	2 Q95L13	Q95L13 ovis aries
17	1140.5	91.2	581	2 Q8UWA9	Q8UWA9 cnemidophor
18	1131.5	90.7	349	1 ESRI_ANOCA	Q9YH33 anolis caro
19	1071.5	85.7	427	2 Q6W5G5	Q6W5G5 xenopus lae
20	1071.5	85.7	427	2 AAQ84784	AAQ84784 xenopus l
21	1071.5	85.7	543	2 Q6W5G9	Q6W5G9 xenopus tro
22	1071.5	85.7	543	2 AAQ84780	AAQ84780 xenopus t
23	1071.5	85.7	585	2 Q6W5G7	Q6W5G7 xenopus lae
24	1071.5	85.7	585	2 AAQ84782	AAQ84782 xenopus l
25	1066.5	85.3	586	1 ESRI_XENLA	P81559 xenopus lae
26	1062.5	85.0	427	2 Q6W5G6	Q6W5G6 xenopus lae
27	1062.5	85.0	427	2 AAQ84783	AAQ84783 xenopus l
28	1025.5	82.0	307	1 ESRI_CNEUN	Q91424 cnemidophor
29	861.5	68.9	174	1 ESRI_BOVIN	F49884 bos taurus
30	824.5	66.0	570	2 Q80Q02	Q80Q02 zoarces viv
31	820.5	65.6	574	2 Q7T2K8	Q7T2K8 halichoeres

32	820.5	65.6	627	2	Q9DDZ4	Q9ddz4 micropterus
33	820.5	65.6	627	2	AAG44622	Aag44622 micropterus
34	818	65.4	542	2	Q90ZE6	Q90ze6 squallus aca
35	812.5	65.0	620	2	Q7SZ10	Q7sz10 fundulus he
36	809.5	64.8	581	1	ESRI_PAGNA	P42132 pagrus majo
37	808.5	64.7	525	1	ESRI_MICUN	P57753 micropogoni
38	808.5	64.7	579	1	ESRI_SPAAU	Q9pv29 sparus aua
39	804.5	64.4	620	1	ESRI_ORYLA	P50241 oryzias lat
40	801.5	64.1	583	2	Q804Q6	Q804q6 acanthopagr
41	801.5	64.1	622	1	ESRI_ONCMY	P16058 oncorhynch
42	798.5	63.9	585	1	ESRI_ORENI	Q9yh33 oreochromis
43	797.5	63.8	535	1	ESRI_SALSA	P50242 salmo salar
44	797	63.8	578	2	Q8QHL0	Q8qhl0 paralichth
45	794.5	63.6	569	1	ESRI_BRARE	P57717 brachydanio

## ALIGNMENTS

RESULT 1	ESRI_HUMAN	STANDARD;	PRT:	595 AA.
ID	ESRI_HUMAN	Q13511; Q14276; Q9NUS1; Q9UDZ7; Q9UIS7;		
AC	P03372; Q13511; Q14276; Q9NUS1; Q9UDZ7; Q9UIS7;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).			
GN	Name=ESR1; Synonyms=NR3A1, ESR;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM LONG).			
RX	MDL=86142927; PubMed=3753802;			
RA	Greene G.L., Galna P., Waterfield M., Baker A., Hort Y., Shine J.;			
RT	"Sequence and expression of human estrogen receptor complementary			
RT	DNA.";			
RL	Science 231:1150-1154 (1986).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM LONG).			
RX	MDL=86146892; PubMed=3754034;			
RA	Green S., Walter P., Kumar V., Krust A., Bornert J.-M., Argos P.,			
RT	Chambon P.;			
RT	"Human oestrogen receptor cDNA: sequence, expression and homology to			
RT	v-erb-A.";			
RL	Nature 320:134-139 (1986).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANT ASP-411 INS.			
RC	TISSUE=Breast;			
RX	MDL=96174665; PubMed=8600466;			
RA	Pink J.J., Wu S.Q., Wolf D.M., Billimoria M.M., Jordan V.C.;			
RT	"A novel 80 kDa human estrogen receptor containing a duplication of			
RT	exons 6 and 7.";			
RL	Nucleic Acids Res. 24:962-969 (1996).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANT SER-77.			
RA	Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,			
RA	Miyamoto K.B., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,			
RA	Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;			
RT	"NIHES-SNPs, environmental genome project, NIHES ES15478, Department			
RT	of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";			
RT	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE OF 152-595 FROM N.A. (ISOFORM LONG).			
RX	MDL=20084372; PubMed=10619354;			
RA	Schubert E.L., Lee M.K., Newman B., King M.C.;			
RT	"Single nucleotide polymorphisms (SNPs) in the estrogen receptor gene			
RT	and breast cancer susceptibility.";			
RL	J. Steroid Biochem. Mol. Biol. 71:21-27 (1999).			
RN	[6]			
RP	TISSUE=Breast carcinoma;			
RC	SEQUENCE OF 216-434 FROM N.A., AND ALTERNATIVE SPLICING.			

RX MEDLINE=93153765; PubMed=7916651;  
RA Pfeiffer U., Pecarotta E., Castagnetta L., Vidali G.;  
RT "Estrogen receptor variant messenger RNA lacking exon 4 in estrogen-  
RT responsive human breast cancer cell lines.";   
RL Cancer Res. 53:741-743(1993).  
RN [7]  
RP SEQUENCE OF 110-117, PHOSPHORYLATION, AND MUTAGENESIS.  
RX MEDLINE=96026869; PubMed=7476978;  
RA Joel P.B., Traish A.M., Lannigan D.A.;  
RT "Estradiol and phorbol ester cause phosphorylation of serine 118 in  
RT the human estrogen receptor.";   
RL Mol. Endocrinol. 9:1041-1052(1995).  
RN [8]  
RP SEQUENCE OF 354-548 FROM N.A.  
RC TISSUE=Breast carcinoma;  
RA Naundorf H., Becker M., Fiebig C., Buettner B., Fichtner I.;  
RT "Mechanisms of acquired tamoxifen resistance in a xenotransplanted  
RT human breast carcinoma.";   
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP SEQUENCE OF 413-595 FROM N.A.  
RA Parker A.;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE OF 532-542, AND PHOSPHORYLATION.  
RX MEDLINE=95280953; PubMed=7539106;  
RA Arnold S.F., Obourn J.D., Jaffe H., Notides A.C.;  
RT "Phosphorylation of the human estrogen receptor on tyrosine 537 in  
RT vivo and by src family tyrosine kinases in vitro.";   
RL Mol. Endocrinol. 9:24-33(1995).  
RN [11]  
RP INTERACTION WITH NCOA6.  
RX MEDLINE=20036574; PubMed=10567404;  
RA Lee S.-K., Anzick S.L., Choi J.-E., Bubendorf L., Guan X.-Y.,  
RA Jung Y.-K., Kallioniemi O.P., Kononen J., Trent J.M., Azorsa D.,  
RA Jhun B.-H., Cheong J.H., Lee Y.C., Meltzer P.S., Lee J.W.;  
RT "A nuclear factor ASC-2, as a cancer-amplified transcriptional  
RT coactivator essential for ligand-dependent transactivation by nuclear  
RT receptors in vivo.";   
RL J. Biol. Chem. 274:34283-34293(1999).  
RN [12]  
RP INTERACTION WITH NCOA5.  
RX MEDLINE=20565767; PubMed=11113208; DOI=10.1128/MCB.21.1.343-353.2001;  
RA Sauve F., McBroom L.D.B., Gallant J., Moraitis A.N., Labrie F.,  
RA Giguere V.;  
RT "CIA, a novel estrogen receptor coactivator with a bifunctional  
RT nuclear receptor interacting determinant.";   
RL Mol. Cell. Biol. 21:343-353(2001).  
RN [13]  
RP PHOSPHORYLATION.  
RX MEDLINE=95140025; PubMed=7838153;  
RA Arnold S.F., Obourn J.D., Jaffe H., Notides A.C.;  
RT "Serine 167 is the major estradiol-induced phosphorylation site on the  
RT human estrogen receptor.";   
RL Mol. Endocrinol. 8:1208-1214(1994).  
RN [14]  
RP PHOSPHORYLATION SITES SER-104 AND SER-106, AND MUTAGENESIS.  
RX MEDLINE=99357754; PubMed=10428798;  
RA Rogatsky I., Trowbridge J.M., Garabedian M.J.;  
RT "Potentiation of human estrogen receptor alpha transcriptional  
RT activation through phosphorylation of serines 104 and 106 by the  
RT cyclin A-CDK2 complex.";   
RL J. Biol. Chem. 274:22296-22302(1999).  
RN [15]  
RP STRUCTURE BY NMR OF 180-262.  
RX MEDLINE=91061891; PubMed=2247153;  
RA Schwabe J.W.E., Neuhaus D., Rhodes D.;  
RT "Solution structure of the DNA-binding domain of the oestrogen  
RT receptor.";   
RL Nature 348:458-461(1990).  
RN [16]  
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 180-262.  
RX MEDLINE=94037103; PubMed=8221895;  
RN [17]  
RX Schwabe J.W.E., Chapman L., Finch J.T., Rhodes D.;  
RT "The crystal structure of the estrogen receptor DNA-binding domain  
RT bound to DNA: how receptors discriminate between their response  
RT elements.";   
RL Cell 75:567-578(1993).  
RN [17]  
RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF 305-548.  
RX MEDLINE=97478539; PubMed=9338790;  
RA Brzozowski A.M., Pike A.C.W., Dauter Z., Hubbard R.E., Bonn T.,  
RA Engstrom O., Oehman L., Greene G.L., Gustafsson J.-A., Carlquist M.;  
RT "Molecular basis of agonism and antagonism in the oestrogen  
RT receptor.";   
RL Nature 389:753-758(1997).  
RN [18]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 306-544.  
RX MEDLINE=98263297; PubMed=9600906;  
RA Tanenbaum D.M., Wang Y., Williams S.P., Sigler P.B.;  
RT "Crystallographic comparison of the estrogen and progesterone  
RT receptor's ligand binding domains.";   
RL Proc. Natl. Acad. Sci. U.S.A. 95:5998-6003(1998).  
RN [19]  
RP X-RAY CRYSTALLOGRAPHY (1.90 ANGSTROMS) OF 294-554.  
RX MEDLINE=99091051; PubMed=9875847;  
RA Shiau A.K., Barstad D., Loria P.M., Cheng L., Kushner P.J.,  
RA Agard D.A., Greene G.L.;  
RT "The structural basis of estrogen receptor/coactivator recognition and  
RT the antagonism of this interaction by tamoxifen.";   
RL Cell 95:927-937(1998).  
RN [20]  
RP 3D-STRUCTURE MODELING OF 311-547.  
RX MEDLINE=98280806; PubMed=9619507;  
RA Maalouf G.J., Xu W., Smith T., Mohr S.C.;  
RT "Homology model for the ligand-binding domain of the human estrogen  
RT receptor.";   
RL J. Biomol. Struct. Dyn. 15:841-850(1998).  
RN [21]  
RP VARIANT VAL-400.  
RX MEDLINE=90005402; PubMed=2792078;  
RA Tori L., Mullick A., Metzger D., Ponglikitmongkol M., Park I.,  
RA Chambon P.;  
RT "The cloned human oestrogen receptor contains a mutation which alters  
RT its hormone binding properties.";   
RL EMBO J. 8:1981-1986(1989).  
RN [22]  
RP VARIANT ALA-447.  
RX MEDLINE=92250650; PubMed=1577818;  
RA Reese J.C., Katzenellenbogen B.S.;  
RT "Characterization of a temperature-sensitive mutation in the hormone  
RT binding domain of the human estrogen receptor. Studies in cell  
RT extracts and intact cells and their implications for hormone-dependent  
RT transcriptional activation.";   
RL J. Biol. Chem. 267:9868-9873(1992).  
RN [23]  
RP VARIANT GLU-364.  
RX MEDLINE=97120591; PubMed=8961262;  
RA McInerney B.M., Ince B.A., Shapiro D.J., Katzenellenbogen B.S.;  
RT "A transcriptionally active estrogen receptor mutant is a novel type  
RT of dominant negative inhibitor of estrogen action.";   
RL Mol. Endocrinol. 10:1519-1526(1996).  
RN [24]  
RP VARIANT CYS-160.  
RX MEDLINE=97338667; PubMed=9195227;  
RA Anderson T.I., Wooster R., Laake K., Collins N., Warren W., Skrede M.,  
RA Beles R., Tveit K.M., Johnston S.R.D., Dowsett M., Olsen A.O.,  
RA Moeller P., Stratton M.R., Boerresen-Dale A.-L.;  
RT "Screening for ESR mutations in breast and ovarian cancer patients.";   
RL Hum. Mutat. 9:531-536(1997).  
CC -!- FUNCTION: Nuclear hormone receptor. The steroid hormones and their  
CC receptors are involved in the regulation of eukaryotic gene  
CC expression and affect cellular proliferation and differentiation  
CC in target tissues.  
CC -!- SUBUNIT: Binds DNA as a homodimer. Interacts with NCOA3, NCOA5 and  
CC Can form a heterodimer with ESR2.

CC NCOA6 coactivators, leading to a strong increase of transcription  
CC of target genes.

Query Match 99.2%; Score 1239.5; DB 1; Length 595;  
Best Local Similarity 99.6%; Pred. No. 1.7e-95;  
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SLALSFLADQMVSAALLDABPILYSEYDPTFPFSEASMMGLLTNLADRELVHMINWAKRV 60  
|||  
Db 305 SLALSFLADQMVSAALLDABPILYSEYDPTFPFSEASMMGLLTNLADRELVHMINWAKRV 364  
|||

Qy 61 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNQGKCVGMEI 120  
|||  
Db 365 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNQGKCVGMEI 424  
|||

Qy 121 FDMLLATSSRPRMNNLOQ-EFVCLKSIILLNSGVYTFLLSSTLKSLSEKDHHRVLDKITT 179  
|||  
Db 425 FDMLLATSSRPRMNNLOQEEFVCLKSIILLNSGVYTFLLSSTLKSLSEKDHHRVLDKITT 484  
|||

Qy 180 TLHLMKAKGLTLQQQHQRLAQLLLIISHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 239  
|||  
Db 485 TLHLMKAKGLTLQQQHQRLAQLLLIISHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 544  
|||

Qy 240 DAHRL 244  
|||  
Db 545 DAHRL 549  
|||

RESULT 2  
ID Q6QIS5 PRELIMINARY; PRT; 596 AA.

AC Q6QIS5;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Estrogen receptor alpha.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Uterus;  
RA Nishimura N., Tetsuka M.;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family.  
DR EMBL; AY538775; AAS46251.1; -;  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR000536; Hrmn\_recept\_lig.  
DR InterPro; IPR001292; Oestrgn\_receptor.  
DR InterPro; IPR001723; Stdhrmn\_receptor.  
DR InterPro; IPR008946; Scr\_ncl\_receptor.  
DR InterPro; IPR001628; Znf\_C4steroid.  
DR Pfam; PF00104; Hormone\_recep; 1.  
DR Pfam; PF02159; Oest\_recep; 1.  
DR Pfam; PF00105; zf-C4; 1.  
DR PRINTS; PR00543; OESTROGENR.  
DR PRINTS; PR00398; STRDHORMONER.  
DR PRINTS; PR00047; STROIDFINGER.  
DR PRODOM; PD000035; Znf\_C4steroid; 1.  
DR SMART; SM00430; HOL1; 1.  
DR SMART; SM00399; Znf\_C4; 1.  
DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
KW DNA-binding; Metal-binding; Nuclear protein; Receptor;  
KW Transcription regulation; Zinc; Zinc-finger.  
SQ SEQUENCE 596 AA; 66489 MW; 3E2CE85BE7844F2 CRC64;

Query Match 96.4%; Score 1205.5; DB 2; Length 596;  
Best Local Similarity 95.9%; Pred. No. 1.2e-92;  
Matches 235; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Estrogen receptor (ER) (Estrogen receptor) (ER-alpha).  
 GN Name=Esrl; Synonyms=Nr3a1, ESR, Estr, Estra;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RC MEDLINE=91042558; PubMed=2484714;  
 RA White R., Lees J.A., Needham M., Ham J., Parker M.;  
 RA "Structural organization and expression of the mouse estrogen  
 RT receptor.";  
 RL Mol. Endocrinol. 1:735-744 (1987).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Bone, and Thymus;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Kazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikiado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami H., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Gough J.,  
 RA Grimond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagahama T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynnshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki J., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RA "Analysis of the mouse transcriptome based on functional annotation of  
 RT 10,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 RN [3]  
 RN SEQUENCE OF 1-22 FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Liver;  
 RX MEDLINE=20359284; PubMed=10899303;  
 RA Kos M., O'Brien S., Flouriot G., Gannon F.;  
 RA "Tissue-specific expression of multiple mRNA variants of the mouse  
 RT estrogen receptor alpha gene.";  
 RL FEBS Lett. 477:15-20 (2000).  
 RN [4]  
 RN SEQUENCE OF 269-599 FROM N.A.  
 RC STRAIN=SJL/J, and B10.S/J; TISSUE=Spleen;  
 RA Ma R.Z., Teuscher C.;  
 RA "Screening for candidate genes of mouse autoimmune diseases.";  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RN CARBOHYDRATE-LINKAGE SITE SER-575.  
 RX MEDLINE=97153020; PubMed=8999954;  
 RA Jiang M.S., Hart G.W.;  
 RA "A subpopulation of estrogen receptors are modified by O-linked N-  
 RT acetylglucosamine.";  
 RL J. Biol. Chem. 272:2421-2428 (1997).  
 RN [6]  
 RN CARBOHYDRATE-LINKAGE SITES SER-10; THR-50 AND SER-575.  
 RX MEDLINE=21124487; PubMed=11226831;  
 RA Cheng X., Hart G.W.;  
 RA "Glycosylation of the murine estrogen receptor-alpha.";  
 RL J. Steroid Biochem. Mol. Biol. 75:147-158 (2000).  
 RN [7]  
 RN INTERACTION WITH NCOA3.  
 RX MEDLINE=97336097; PubMed=9192892;  
 RA Torchia J., Rose D.W., Inostroza J., Kamei Y., Westin S., Glass C.K.,  
 RA Rosenfeld M.G.;  
 RA "The transcriptional co-activator p/CIP binds CBP and mediates  
 RT nuclear-receptor function.";  
 RL Nature 387:677-684 (1997).  
 RN [8]  
 RN INTERACTION WITH NCOA6.  
 RX MEDLINE=2050907; PubMed=10788465;  
 RA Zhu Y.-J., Kan L., Qi C., Kanwar Y.S., Yeldandi A.V., Rao M.S.,  
 RA Reddy J.K.;  
 RA "Isolation and characterization of peroxisome proliferator-activated  
 RT receptor (PPAR) interacting protein (PRIP) as a coactivator for  
 RT PPAR.";  
 RL J. Biol. Chem. 275:13510-13516 (2000).  
 CC -!- FUNCTION: Nuclear hormone receptor. The steroid hormones and their  
 CC receptors are involved in the regulation of eukaryotic gene  
 CC expression and affect cellular proliferation and differentiation  
 CC in target tissues.  
 CC -!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with  
 CC ESR2. Interacts with NCOA3 and NCOA6 coactivators, leading to a  
 CC strong increase of transcription of target genes. Interacts with  
 CC NCOA5. Binds UBE1C (by similarity).  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,  
 CC a DNA-binding domain and a C-terminal steroid-binding domain.  
 CC -!- PTM: Phosphorylated by cyclin A/CDK2 (by similarity).  
 CC -!- MISCELLANEOUS: In the absence of ligand, steroid hormone receptors  
 CC are thought to be weakly associated with nuclear components;  
 CC hormone binding greatly increases receptor affinity. The hormone-  
 CC receptor complex appears to recognize discrete DNA sequences  
 CC upstream of transcriptional start sites.  
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3  
 CC subfamily.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M38651; AAA37580.1; -;  
 CC EMBL; AK036627; BAC29510.1; -;  
 CC EMBL; AK041525; BAC30973.1; -;  
 CC EMBL; AJ276597; CAB85618.1; -;  
 CC EMBL; AF128221; AAF22562.1; -;  
 CC EMBL; AF128220; AAF22561.1; -;  
 CC PIR; A40061; QRMSE.  
 CC HSP; P03372; LHCF.  
 CC TRANSFAC; T00259; -;  
 CC GlycoSuiteDB; P19785; -;  
 CC MGD; MGI:1352467; Esrl.  
 CC GO; GO:0016585; C:chromatin remodeling complex; ISS.  
 CC GO; GO:0005737; C:cytoplasm; IDA.  
 CC GO; GO:0016020; C:membrane; ISS.  
 CC GO; GO:0005634; C:nucleus; IDA.  
 CC GO; GO:0030284; F:estrogen receptor activity; ISS.  
 CC GO; GO:0030235; F:nitric-oxide synthase regulator activity; ISS.  
 CC GO; GO:0016049; P:cell growth; NAS.  
 CC GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.  
 CC GO; GO:0045839; P:negative regulation of mitosis; NAS.  
 CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.  
 CC InterPro; IPR000536; Hrmn\_recept\_lig.  
 CC InterPro; IPR001292; Oestrgn\_receptor.  
 CC InterPro; IPR001723; Stdhrmn\_receptor.  
 CC InterPro; IPR008946; Str\_ncl\_receptor.



```

DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Phosphorylation; Receptor;
FT DOMAIN 1 189 Modulating.
FT DNA_BIND 190 255 Nuclear receptor-type.
FT ZN_FING 190 210 C4-type.
FT ZN_FING 226 250 C4-type.
FT DOMAIN 256 315 Hinge.
FT DOMAIN 316 600 Steroid-binding.
FT DOMAIN 64 71 Poly-Ala.
FT DOMAIN 171 174 Poly-Ser.
FT MOD_RES 109 109 Phosphoserine (by CDK2) (By similarity).
FT MOD_RES 111 111 Phosphoserine (by CDK2) (By similarity).
FT MOD_RES 123 123 Phosphoserine (By similarity).
FT MOD_RES 172 172 Phosphoserine (by CK2) (By similarity).
FT MOD_RES 542 542 Phosphotyrosine (by Tyr-kinases) (By similarity).
FT CONFLICT 488 488 N -> T (in Ref. 3).
SQ SEQUENCE 600 AA; 67030 MW; C9C7D8CACE0F57D8 CRC64;

Match
Best Local Similarity 96.0%; Score 1200.5; DB 1; Length 600;
Matches 235; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 1 SLALSITADQVMSALLDAPPLIYSEYDTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
DB 310 SPALSITADQVMSALLDAPPLIYSEYDTRPFSEASMMGLLTNLADRELVHMINWAKRV 369
QY 61 PGFVDLTLDQVHLLCAWLEIMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEVI 120
DB 370 PGFGDLNLDQVHLLCAWLEIMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEVI 429
QY 121 FQMLLATSSRRFMNLIQG-EFVCLKSIILLNSGVYFLSSTLKSLEEKDHHRVLDKIND 179
DB 430 FQMLLATSSRRFMNLIQGEFVCLKSIILLNSGVYFLSSTLKSLEEKDHHRVLDKIND 489
QY 180 TLHLMAKAGLTQQQHQRLAQALLTLSHIRHMSNKGMEHLYSMCKKNVVPYDYLLEML 239
DB 490 TLHLMAKAGLTQQQHQRLAQALLTLSHIRHMSNKGMEHLYSMCKKNVVPYDYLLEML 549
QY 240 DAHRL 244
DB 550 DAHRL 554

RESULT 6
ESR1_PIG STANDARD; PRT; 595 AA.
AC 29040;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
GN Name=ESR1; Synonyms=NR3A1, ESR;
OS Sus scrofa (Pig);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Uterus;
RX MEDLINE=95080454; PubMed=7998744;
RA Boekenkamp D., Jungblut P.W., Thole H.H.;
RT "The C-terminal half of the porcine estradiol receptor contains no
RT post-translational modification: determination of the primary
RT structure.";
RL Mol. Cell. Endocrinol. 104:163-172(1994).
CC -!- FUNCTION: Nuclear hormone receptor. The steroid hormones and their
CC receptors are involved in the regulation of eukaryotic gene
CC expression and affect cellular proliferation and differentiation
CC in target tissues (By similarity).
CC -!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with
CC ESR2. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading

```

```

CC to a strong increase of transcription of target genes. Binds UBE1C
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC -!- PTM: Phosphorylated by cyclin A/CDK2 (By similarity).
CC -!- MISCELLANEOUS: In the absence of ligand, steroid hormone receptors
CC are thought to be weakly associated with nuclear components;
CC hormone binding greatly increases receptor affinity. The hormone-
CC receptor complex appears to recognize discrete DNA sequences
CC upstream of transcriptional start sites.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z37167; CAA85524.1; -.
CC F01R; I47140; I47140.
CC HSP; P03372; IHCP.
CC GO; GO:0016585; C:chromatin remodeling complex; ISS.
CC GO; GO:0016020; C:membrane; ISS.
CC GO; GO:0030284; F:estrogen receptor activity; ISS.
CC GO; GO:0030233; F:nitric-oxide synthase regulator activity; ISS.
CC GO; GO:0016049; P:cell growth; ISS.
CC GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.
CC GO; GO:0045839; P:negative regulation of mitosis; ISS.
CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
CC InterPro; IPR000536; Hmon_recept_lig.
CC InterPro; IPR001292; Oestrgn_receptor.
CC InterPro; IPR001723; Strdhmn_receptor.
CC InterPro; IPR008946; Str_ncl_receptor.
CC InterPro; IPR001628; Znf_C4steroid.
CC Pfam; PF00104; Hormone_recep; 1.
CC Pfam; PF02159; Oest_recep; 1.
CC Pfam; PF00105; zf-C4; 1.
CC PRINTS; PR00543; OESTROGENR.
CC PRINTS; PR00398; STRDHOMONER.
CC PRINTS; PR00047; STROIDFINGER.
CC ProDom; PD000035; Znf_C4steroid; 1.
CC SMART; SM00430; HOLI_1.
CC SMART; SM00399; Znf_C4; 1.
CC PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
KW Direct protein sequencing; DNA-binding; Nuclear protein;
KW Phosphorylation; Receptor; Steroid-binding; Transcription regulation;
KW Zinc-finger.
FT DOMAIN 1 184 Modulating.
FT DNA_BIND 185 250 Nuclear receptor-type.
FT ZN_FING 185 205 C4-type.
FT ZN_FING 221 245 C4-type.
FT DOMAIN 251 310 Hinge.
FT DOMAIN 311 551 Steroid-binding.
FT DOMAIN 64 70 Poly-Ala.
FT MOD_RES 104 104 Phosphoserine (by CDK2) (By similarity).
FT MOD_RES 106 106 Phosphoserine (by CDK2) (By similarity).
FT MOD_RES 118 118 Phosphoserine (By similarity).
FT MOD_RES 167 167 Phosphoserine (by CK2) (By similarity).
FT MOD_RES 537 537 Phosphotyrosine (by Tyr-kinases) (By similarity).
SQ SEQUENCE 595 AA; 66361 MW; 0EC23DC3085BF001 CRC64;

Query Match 95.8%; Score 1197.5; DB 1; Length 595;
Best Local Similarity 95.1%; Pred. No. 5.7e-92;
Matches 233; Conservative 7; Mismatches 4; Indels 1; Gaps 1;

QY 1 SLALSITADQVMSALLDAPPLIYSEYDTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
DB 305 SPVLSLTADQMISALLEAPPLIYSEYDTRPLSEASMMGLLTNLADRELVHMINWAKRV 364

```

QY 61 PGFVDLTLDHVDHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 120  
 DB 365 PGFLDLSLDHVDHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 424  
 QY 121 FDMLLATSSRRFRMMNLQ-EPVCLKSIILLNSGVYTFLLSSTLKSLEKDHHRVLDKITD 179  
 DB 425 FDMLLATSSRRFRMMNLQ-EPVCLKSIILLNSGVYTFLLSSTLKSLEKDHHRVLDKITD 484  
 QY 180 TLIHMAKAGLTQQOQHRLAQLLLSHIRHMSNKGMEHLYSMKCNVVPYDILLLEML 239  
 DB 485 TLIHMAKAGLTQQOQHRLAQLLLSHIRHMSNKGMEHLYSMKCNVVPYDILLLEML 544  
 QY 240 DAHRL 244  
 DB 545 DAHRL 549

RESULT 7  
 ESTER1 MESAU STANDARD; PRT; 595 AA.  
 AC Q9QZJ5; Q9QZG6;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).  
 GN Name=ESR1; Synonyms=NR3A1, ESR;  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RA MEDLINE=20197937; PubMed=10731637;  
 RA Bhat H.K., Vadgama J.V.;  
 RL "Hamster estrogen receptor cDNA: cloning and mRNA expression.";  
 RN J. Steroid Biochem. Mol. Biol. 72:47-53(2000).  
 RP [2]  
 RP SEQUENCE OF 98-291 FROM N.A.  
 RA Jones J.E., Carpenter C.D., Lubbers L.S., Petersen S.L., Wade G.N.;  
 RT "Return of lordosis after food deprivation and refeeding in Syrian hamsters.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Nuclear hormone receptor. The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues (By similarity).  
 CC -!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with ESR2. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading to a strong increase of transcription of target genes. Binds UBE1C (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.  
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3 subfamily.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF181077; AAD53956.1; -;  
 CC EMBL; AF184276; AAF02721.1; -;  
 CC HSSP; P03372; 1HCQ  
 DR GO; GO:0016585; C:chromatin remodeling complex; ISS.  
 DR GO; GO:0016020; C:membrane; ISS.  
 DR GO; GO:0030284; F:estrogen receptor activity; ISS.

DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; ISS.  
 DR GO; GO:0016049; P:cell growth; ISS.  
 DR GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.  
 DR GO; GO:0045839; P:negative regulation of mitosis; ISS.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.  
 DR InterPro; IPR000536; Hrmn\_recept\_lig.  
 DR InterPro; IPR001292; Sterhmn\_receptor.  
 DR InterPro; IPR008946; Str\_ncl\_receptor.  
 DR InterPro; IPR001628; Znf\_C4steroid.  
 DR Pfam; PF00104; Hormone\_recep; 1.  
 DR Pfam; PF02159; Oest\_recep; 1.  
 DR Pfam; PF00105; zf-C4; 1.  
 DR PRINTS; PR00543; OESTROGENR.  
 DR PRINTS; PR00398; STRDHORMONER.  
 DR PRINTS; PR00047; STROIDFINGER.  
 DR ProDom; PD000035; Znf\_C4steroid; 1.  
 DR SMART; SM00430; HOL1; 1.  
 DR SMART; SM00399; Znf\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.  
 KW DNA-binding; Nuclear protein; Phosphorylation; Receptor;  
 KW Steroid-binding; Transcription regulation; Zinc-finger.  
 FT DOMAIN 1 184  
 FT DNA\_BIND 185 250  
 FT ZN\_FING 185 205  
 FT ZN\_FING 221 245  
 FT DOMAIN 251 310  
 FT DOMAIN 311 551  
 FT DOMAIN 112 115  
 FT DOMAIN 166 169  
 FT MOD\_RES 103 103  
 FT MOD\_RES 105 105  
 FT MOD\_RES 118 118  
 FT MOD\_RES 167 167  
 FT MOD\_RES 537 537  
 FT CONFLICT 98 99  
 FT CONFLICT 144 144  
 FT CONFLICT 198 199  
 FT CONFLICT 290 291  
 SQ SEQUENCE 595 AA; 66833 MW; E4D803B4FFDB257E CRC64;  
 Query Match 95.4%; Score 1192.5; DB 1; Length 595;  
 Best Local Similarity 94.7%; Pred. No. 1.5e-91;  
 Matches 232; Conservative 8; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 SLALSITADQVSGALLDAEPPIYSEYDTPRPSEASMMGLLTNLADRELVHMINNAKRV 60  
 DB 305 SPALSITADQVSGALLDAEPPIYSEYDTPRPSEASMMGLLTNLADRELVHMINNAKRV 364  
 QY 61 PGFVDLTLDHVDHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 120  
 DB 365 PGFVDLTLDHVDHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 424  
 QY 121 FDMLLATSSRRFRMMNLQ-EPVCLKSIILLNSGVYTFLLSSTLKSLEKDHHRVLDKITD 179  
 DB 425 FDMLLATSSRRFRMMNLQ-EPVCLKSIILLNSGVYTFLLSSTLKSLEKDHHRVLDKITD 484  
 QY 180 TLIHMAKAGLTQQOQHRLAQLLLSHIRHMSNKGMEHLYSMKCNVVPYDILLLEML 239  
 DB 485 TLIHMAKAGLTQQOQHRLAQLLLSHIRHMSNKGMEHLYSMKCNVVPYDILLLEML 544  
 QY 240 DAHRL 244  
 DB 545 DAHRL 549

RESULT 8  
 Q8UWB0  
 ID Q8UWB0 PRELIMINARY; PRT; 587 AA.  
 AC Q8UWB0;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

```

DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Estrogen receptor.
OS Caiman crocodilus (Spectacled caiman) (Caiman sclerops).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Caiman.
OX NCBI_TaxID=8499;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21490797; PubMed=11604222;
RA Sumida K., Ooe N., Saito K., Kaneko H.;
RT "Molecular cloning and characterization of reptilian estrogen receptor
CDNA."
RL Mol. Cell. Endocrinol. 183:33-39 (2001).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AB055220; BAB79436.1; -.
DR HSSP; P03372; 1HCP.
DR GO; GO:0016020; C:membrane; ISS.
DR GO; GO:0030284; F:estrogen receptor activity; ISS.
DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; ISS.
DR GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
DR InterPro; IPR000536; Hrmn_recept_lig.
DR InterPro; IPR001292; Oestrn_recept.
DR InterPro; IPR001723; Stdrnm_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00543; OESTROGENR.
DR PRINTS; PR00398; STRODHORMNER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Phosphorylation; Receptor;
KW Steroid-binding; Transcription regulation; Zinc-finger.
FT DOMAIN 1 184 Modulating.
FT DNA_BIND 185 250 Nuclear receptor-type.
FT ZN_FING 185 205 C4-type.
FT ZN_FING 221 245 C4-type.
FT DOMAIN 251 310 Hinge.
FT DOMAIN 311 550 Steroid-binding.
FT DOMAIN 64 70 Poly-Ala.
FT MOD_RES 104 104 Phosphoserine (by CDK2) (By similarity).
FT MOD_RES 106 106 Phosphoserine (by CDK2) (By similarity).
FT MOD_RES 118 118 Phosphoserine (by CK2) (By similarity).
FT MOD_RES 167 167 Phosphotyrosine (by Tyr-kinases) (By
FT MOD_RES 536 536 similarity).

DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
GN Name=ESR1; Synonyms=NR3A1, ESR;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX McDowell K.J., Adams M.H., Green M.L., Cleaver B.D., Sharp D.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Nuclear hormone receptor. The steroid hormones and their
CC receptors are involved in the regulation of eukaryotic gene
CC expression and affect cellular proliferation and differentiation
CC in target tissues (By similarity). Can form a heterodimer with
CC ESR2. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading
CC to a strong increase of transcription of target genes.Binds UBE1C
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
CC subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
DR EMBL; AF124093; AAD17316.1; -.
DR HSSP; P03372; 1HCP.
DR GO; GO:0016585; C:chromatin remodeling complex; ISS.
DR GO; GO:0016020; C:membrane; ISS.
DR GO; GO:0030284; F:estrogen receptor activity; ISS.
DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; ISS.
DR GO; GO:0016049; P:cell growth; ISS.
DR GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.
DR GO; GO:0045839; P:negative regulation of mitosis; ISS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
DR InterPro; IPR000536; Hrmn_recept_lig.
DR InterPro; IPR001292; Oestrn_recept.
DR InterPro; IPR001723; Stdrnm_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; Oest_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00543; OESTROGENR.
DR PRINTS; PR00398; STRODHORMNER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 587 AA; 66513 MW; DE17F2B837FCF513 CRC64;

Query Match 94.4%; Score 1179.5; DB 2; Length 587;
Best Local Similarity 93.9%; Pred.No. 1.8e-30;
Matches 230; Conservative 11; Mismatches 3; Indels 1; Gaps 1;

QY 1 SLALSTADQMSYALDAPPIYSEYDTPFPSEASMMGLTLNLADRELVHMINKAKRV 60
Db 299 SPALSLTAQMSYALDAPPIYSEYDTPFPSEASMMGLTLNLADRELVHMINKAKRV 358
QY 61 PGFVDTLHDQVHLLCAWLEILMIGLVRSMEHPGKLLFAPNLLDRNQKCGVEGMVEI 120
Db 359 PGFVDTLHDQVHLLCAWLEILMIGLVRSMEHPGKLLFAPNLLDRNQKCGVEGMVEI 418
QY 121 FDMLLATSRFRMMNLQG-EFVCLKSIIILNSGVYTFLSSTLSKEEDKHHRVLDKIID 179
Db 419 FDMLLATSRFRMMNLQGEFEVCLKSIIILNSGVYTFLSSTLSKEEDKHHRVLDKIID 478
QY 180 TLTIHMAKAGLTQQHQRLAQQLLTLSHIRMSNKGMEHLSMKCKNVVPLYDLLLEML 239
Db 479 TLTIHMAKAGLTQQHQRLAQQLLTLSHIRMSNKGMEHLSMKCKNVVPLYDLLLEML 538
QY 240 DAHRL 244
Db 539 DAHRL 543

RESULT 9
ESR1_HORSE
ID ESR1_HORSE STANDARD; PRT; 594 AA.
AC Q9TV98;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

```



```
SQ SEQUENCE 594 AA; 66103 MW; DD36CA7C24C74B95 CRC64;
Query Match 94.3%; Score 1179; DB 1; Length 594;
Best Local Similarity 94.7%; Pred. No. 2e-90;
Matches 232; Conservative 7; Mismatches 4; Indels 2; Gaps 2;
Qy 1 SLALSLTADQWVSALLDABPPILYSEYDPTPPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SPVLSLTAEQMSALLDABPPILYSEYDPTPPFSEASMMGLLTNLADRELVHMINWAKRV 364
Qy 61 PGFVDLTLDQVHLLCAWLEILMGLVWRSMEHPGKLLFAPNLLLDNRQCKVEGVVEI 120
Db 365 PGFVDLSLHDQVHLLCAWLEILMGLVWRSMEHPGKLLFAPNLLLDNRQCKVEGVVEI 424
Qy 121 FDMLLATSSRFMMNLOG-EFVCLKSIILLNSGYVTFLLSKLSLEEKDHIHRVLDKITD 179
Db 425 FDMLLATSSRLRMNLOGEEFVCLKSIILLNSGYVTFLLSKLSLEEKDHIHRVLDKITD 484
Qy 180 TLIIHMAKAGLTQQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 239
Db 485 TLIIHMAKAGLT-QOHRRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 543
Qy 240 DAHRL 244
Db 544 DAHRL 548
RESULT 10
ESR1_POEGU STANDARD; PRT; 587 AA.
ID _ESR1_POEGU STANDARD; PRT; 587 AA.
AC Q91250;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
GN Name=ESR1; Synonyms=NR3A1, ESR;
OS Poephila guttata (Zebra finch) (Taeniopygia guttata).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;
OC Estrilidae; Taeniopygia.
OX NCBI_TaxID=59729;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Hypothalamus;
RC MEDLINE=97163508; PubMed=9010328;
RA Jacobs E.C., Arnold A.P., Campagnoni A.T.;
RT "Zebra finch estrogen receptor cDNA: cloning and mRNA expression.";
RL 7. Steroid Biochem. Mol. Biol. 59:135-145(1996).
CC - FUNCTION: The steroid hormones and their receptors are involved in
CC the regulation of eukaryotic gene expression and affect cellular
CC proliferation and differentiation in target tissues.
CC - SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with ER-
CC beta (By similarity).
CC - SUBCELLULAR LOCATION: Nuclear.
CC - DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC - SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
CC subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; L79911; AAB81108.1; --
CC HSP; P03372; IHP.
CC DR GO; GO:0016585; C:chromatin remodeling complex; ISS.
CC DR GO; GO:0016020; C:membrane; ISS.
CC DR GO; GO:0030284; F:estrogen receptor activity; ISS.
CC DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; ISS.
```

```
DR GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
DR InterPro; IPR000536; H:hmom recept lig.
DR InterPro; IPR001292; O:estrgn receptor.
DR InterPro; IPR001723; S:cdhrmn receptor.
DR InterPro; IPR008946; S:stdhrmn receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; H:ormone recep; 1.
DR Pfam; PF02159; O:est recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00543; OESTROGENR.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Steroid-binding;
KW Transcription regulation; Zinc-finger.
FT DOMAIN 1 176 Modulating.
FT DNA BIND 177 242 Nuclear receptor-type.
FT ZN_FING 177 197 C4-type.
FT ZN_FING 213 237 C4-type.
FT DOMAIN 243 302 Hinge.
FT DOMAIN 303 587 Steroid-binding.
SQ SEQUENCE 587 AA; 66553 MW; 2B254168A7A910AB CRC64;
Query Match 94.2%; Score 1177.5; DB 1; Length 587;
Best Local Similarity 93.5%; Pred. No. 2.7e-90;
Matches 229; Conservative 12; Mismatches 3; Indels 1; Gaps 1;
Qy 1 SLALSLTADQWVSALLDABPPILYSEYDPTPPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 297 SPALSLTAEQMSALLDABPPILYSEYDPTPPFSEASMMGLLTNLADRELVHMINWAKRV 356
Qy 61 PGFVDLTLDQVHLLCAWLEILMGLVWRSMEHPGKLLFAPNLLLDNRQCKVEGVVEI 120
Db 357 PGFVDLTLDQVHLLCAWLEILMGLVWRSMEHPGKLLFAPNLLLDNRQCKVEGVVEI 416
Qy 121 FDMLLATSSRFMMNLOG-EFVCLKSIILLNSGYVTFLLSKLSLEEKDHIHRVLDKITD 179
Db 417 FDMLLATAARFRMMNLOGEEFVCLKSIILLNSGYVTFLLSKLSLEEKDHIHRVLDKITD 476
Qy 180 TLIIHMAKAGLTQQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 239
Db 477 TLIIHMAKAGLTQQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 536
Qy 240 DAHRL 244
Db 537 DAHRL 541
RESULT 11
ESR1_CHICK STANDARD; PRT; 589 AA.
ID _ESR1_CHICK STANDARD; PRT; 589 AA.
AC P06212;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
GN Name=ESR1; Synonyms=NR3A1, ESR;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=86247578; PubMed=3755102;
RA Krust A., Green S., Argos P., Kumar V., Walter P., Bornert J.-M.,
RA Chambon P.;
RT "The chicken estrogen receptor sequence: homology with v-erbA and the
RT human estrogen and glucocorticoid receptors.";
```

RL EMBO J. 5:891-897(1986).

CC -!- FUNCTION: The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues.

CC -!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with ER-beta.

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.

CC -!- MISCELLANEOUS: In the absence of ligand, steroid hormone receptors are thought to be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone-receptor complex appears to recognize discrete DNA sequences upstream of transcriptional start sites.

CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3 subfamily.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

DR EMBL; X03805; CAA27433.1; --

DR F01; A40914; QRCHE.

DR HSP; P03372; LHCP.

DR TRANSFAC; T00264; --

DR GO; GO:0016585; C:chromatin remodeling complex; ISS.

DR GO; GO:0016020; C:membrane; ISS.

DR GO; GO:0030284; F:estrogen receptor activity; ISS.

DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; ISS.

DR GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.

DR InterPro; IPR000536; Hmon\_recept\_lig.

DR InterPro; IPR001292; Oestrgn\_receptor.

DR InterPro; IPR001723; Stdhrmn\_receptor.

DR InterPro; IPR008946; Str\_ncl\_receptor.

DR Pfam; PF02159; Oest\_recep; 1.

DR Pfam; PF00105; zf-C4; 1.

DR PRINTS; PR00543; OESTROGENR.

DR PRINTS; PR00398; STRDHORMONER.

DR PRINTS; PR00047; STROIDFINGER.

DR ProDom; PD000035; Znf\_C4steroid; 1.

DR SMART; SM00399; ZNF\_C4; 1.

DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.

KW DNA-binding; Nuclear protein; Receptor; Steroid-binding; Transcription regulation; Zinc-finger.

FT DOMAIN 1 178 Modulating.

FT DNA\_BIND 179 244 Nuclear receptor-type.

FT ZN\_FING 179 199 C4-type.

FT ZN\_FING 215 239 C4-type.

FT DOMAIN 245 304 Hinge.

FT DOMAIN 305 589 Steroid-binding.

SQ SEQUENCE 589 AA; 66746 MW; 1B092233C770A54B CRC64;

Query Match 94.1%; Score 1176.5; DB 1; Length 589;

Best Local Similarity 93.5%; Pred. No. 3.3e-90; Indels 1; Gaps 1;

Matches 229; Conservative 12; Mismatches 3;

QY 1 SLALSLTADQWVSALLDAEPPIYSEYDPTFPFSEASMMGLTLNLADRELVHMINWAKRV 60

DB 299 SPALSLTAQWVSALLAEPPVYSEYDPTFPFSEASMMGLTLNLADRELVHMINWAKRV 358

QY 61 PGFVDLTLDQVHLLCAWLEIMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGWEI 120

DB 359 PGFVDLTLDQVHLLCAWLEIMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGWEI 418

QY 121 FDMLLATSSRRFRMNLQGEFVCLSKSIILLNSGVYTFLSSTLSLEEKDHIHRVLDKITYD 179

DB 419 FDMLLATAARFRMNLQGEFVCLSKSIILLNSGVYTFLSSTLSLEEKDYIHRVLDKITYD 478

Db 419 FDMLLATAARFRMNLQGEFVCLSKSIILLNSGVYTFLSSTLSLEEKDYIHRVLDKITYD 478

QY 180 TLIHLMAKAGITLQOQHQRLLAQLLILSHIRMSNKGMEHLYSMKCKNVVPLYDLLEML 239

Db 479 TLIHLMAKSGLSLQOQHRRLLAQLLILSHIRMSNKGMEHLYNMCKCKNVVPLYDLLEML 538

QY 240 DAHRL 244

Db 539 DAHRL 543

RESULT 12

QY65N7 Q765N7 PRELIMINARY; PRT; 587 AA.

AC Q765N7; DT 05-JUL-2004 (TREMELrel. 27, Created)

DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)

DE Estrogen receptor a.

GN Name=Era;

OS Alligator mississippiensis (American alligator).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Crocodylidae; Alligatorinae; Alligator.

OC NCBI\_TaxID=8496;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Gonad;

RX PubMed:14980803;

RA Katsui Y., Bermudez D.S., Braun E.L., Helbing C., Miyagawa S., Gunderson M.P., Kohno S., Bryan T.A., Guillelte L.J., Iguchi T.; "Molecular cloning of the estrogen and progesterone receptors of the American alligator.";

RT Gen. Comp. Endocrinol. 136:122-133 (2004).

RL -!- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.

DR EMBL; AB115909; BAD08348.1; --

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR000536; Hmon\_recept\_lig.

DR InterPro; IPR001292; Oestrgn\_receptor.

DR InterPro; IPR001723; Stdhrmn\_receptor.

DR InterPro; IPR008946; Str\_ncl\_receptor.

DR InterPro; IPR001628; Znf\_C4steroid.

DR Pfam; PF00104; Hormone\_recep; 1.

DR Pfam; PF02159; Oest\_recep; 1.

DR Pfam; PF00105; zf-C4; 1.

DR PRINTS; PR00543; OESTROGENR.

DR PRINTS; PR00398; STRDHORMONER.

DR PRINTS; PR00047; STROIDFINGER.

DR ProDom; PD000035; Znf\_C4steroid; 1.

DR SMART; SM00430; HOLI; 1.

DR SMART; SM00399; ZNF\_C4; 1.

DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.

KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription regulation; Zinc; Zinc-finger.

SQ SEQUENCE 587 AA; 66497 MW; FC217FCC0F1B41F0 CRC64;

Query Match 94.0%; Score 1175.5; DB 2; Length 587;

Best Local Similarity 93.5%; Pred. No. 4e-90; Indels 1; Gaps 1;

Matches 229; Conservative 12; Mismatches 3;

QY 1 SLALSLTADQWVSALLDAEPPIYSEYDPTFPFSEASMMGLTLNLADRELVHMINWAKRV 60

DB 299 SPALSLTAQWVSALLAEPPVYSEYDPTFPFSEASMMGLTLNLADRELVHMINWAKRV 358

QY 61 PGFVDLTLDQVHLLCAWLEIMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGWEI 120

DB 359 PGFVDLTLDQVHLLCAWLEIMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGWEI 418

QY 121 FDMLLATSSRRFRMNLQGEFVCLSKSIILLNSGVYTFLSSTLSLEEKDHIHRVLDKITYD 179

Db 419 FDMLLATAARFRMNLQGEFVCLSKSIILLNSGVYTFLSSTLSLEEKDYIHRVLDKITYD 478

QY 180 TLHLMAKAGLTLQOQHRLAQLLLILSHIRHMSKMGHEHLYSMKCKNVVPLYDLLLLL 239  
 DB 479 TLHLMAKAGLTLQOQHRLAQLLLILSHIRHMSKMGHEHLYSMKCKNVVPLYDLLLLL 538  
 QY 240 DAHRL 244  
 DB 539 DAHRL 543  
 RESULT 13  
 BAD08348 PRELIMINARY; PRT; 587 AA.  
 AC BAD08348;  
 DT 14-APR-2004 (TReMBLrel. 27, Created)  
 DT 14-APR-2004 (TReMBLrel. 27, Last sequence update)  
 DT 14-APR-2004 (TReMBLrel. 27, Last annotation update)  
 DE Estrogen receptor a.  
 GN ERA  
 OS Alligator mississippiensis (American alligator).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Crocodyliidae; Alligatorinae; Alligator.  
 OX NCBI\_TaxID=8496;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Gonad;  
 RA Katsu Y., Bermudez D.S., Braun E.L., Helbing C., Miyagawa S.,  
 RA Gunderson M.P., Kohno S., Bryan T.A., Guillet L.J., Iguchi T.;  
 RT "Molecular cloning of the estrogen and progesterone receptors of the  
 RT American alligator."  
 RL Gen. Comp. Endocrinol. 136:122-133 (2004).  
 KW EMBL; AB115909; BAD08348.1; -.  
 SQ SEQUENCE 587 AA; 66497 MW; FC217FCC0F1B41F0 CRC64;  
 Query Match 94.0%; Score 1175.5; DB 2; Length 587;  
 Best Local Similarity 93.5%; Pred. No. 4e-90;  
 Matches 229; Conservative 12; Mismatches 3; Indels 1; Gaps 1;  
 QY 1 SLALSTADQVMSALLDAEPPILYSEYDPTFPFSEASNMGLLTNLADRELVHMINWAKRV 60  
 DB 299 SPALSLTAEQVMSALLAEPPIVYSEYDNPFPNEASMTLLTNLADRELVHMINWAKRV 358  
 QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGEMVEI 120  
 DB 359 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGEMVEI 418  
 QY 121 FDMLLATSSFRMNLQGFVCLKSIILLNSGVYTFLSSTLSLEEKDTHRVLDKITD 179  
 DB 419 FDMLLATAARFRMNLQGFVCLKSIILLNSGVYTFLSSTLSLEEKDTHRVLDKITD 478  
 QY 180 TLHLMAKAGLTLQOQHRLAQLLLILSHIRHMSKMGHEHLYSMKCKNVVPLYDLLLLL 239  
 DB 479 TLHLMAKAGLTLQOQHRLAQLLLILSHIRHMSKMGHEHLYSMKCKNVVPLYDLLLLL 538  
 QY 240 DAHRL 244  
 DB 539 DAHRL 543  
 RESULT 14  
 Q8AYHO PRELIMINARY; PRT; 589 AA.  
 AC Q8AYHO;  
 DT 01-MAR-2003 (TReMBLrel. 23, Created)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Estrogen receptor alpha.  
 GN Coturnix coturnix japonica (Japanese quail).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Coturnix.  
 OX NCBI\_TaxID=93934;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Ichikawa K., Yamamoto I., Tsukada A., Saito N., Shimada K.;  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family.  
 DR EMBL; AF442965; AANG3674.1; -.  
 DR HSSP; P03372; IHCP.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0005496; F:steroid hormone receptor activity; IEA.  
 DR GO; GO:0003707; F:steroid hormone receptor activity; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR000536; Hrmn\_recept\_lig.  
 DR InterPro; IPR001292; Oestrgn\_receptor.  
 DR InterPro; IPR001723; Strdhmn\_receptor.  
 DR InterPro; IPR008946; Str\_ncl\_receptor.  
 DR InterPro; IPR001628; Znf\_C4steroid.  
 DR Pfam; PF00104; Hormone\_recep; 1.  
 DR Pfam; PF02159; Oest\_recep; 1.  
 DR Pfam; PF00105; zf-C4; 1.  
 DR PRINTS; PR00543; OESTROGENR.  
 DR PRINTS; PR00398; STRDHMONER.  
 DR PRINTS; PR00047; STROIDFINGER.  
 DR ProDom; PD000035; Znf\_C4steroid; 1.  
 DR SMART; SM00430; HOL1; 1.  
 DR SMART; SM00399; Znf C4; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
 KW DNA-binding; Metal-binding; Nuclear protein; Receptor;  
 KW Transcription regulation; Zinc; Zinc-finger.  
 SQ SEQUENCE 589 AA; 66767 MW; 8271PDAA67552CA4 CRC64;  
 Query Match 93.8%; Score 1172.5; DB 2; Length 589;  
 Best Local Similarity 93.1%; Pred. No. 7.1e-90;  
 Matches 228; Conservative 12; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 SLALSTADQVMSALLDAEPPILYSEYDPTFPFSEASNMGLLTNLADRELVHMINWAKRV 60  
 DB 299 SPALSLTAEQVMSALLAEPPIVYSEYDNPFPNEASMTLLTNLADRELVHMINWAKRV 358  
 QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGEMVEI 120  
 DB 359 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGEMVEI 418  
 QY 121 FDMLLATSSFRMNLQGFVCLKSIILLNSGVYTFLSSTLSLEEKDTHRVLDKITD 179  
 DB 419 FDMLLATAARFRMNLQGFVCLKSIILLNSGVYTFLSSTLSLEEKDTHRVLDKITD 478  
 QY 180 TLHLMAKAGLTLQOQHRLAQLLLILSHIRHMSKMGHEHLYSMKCKNVVPLYDLLLLL 239  
 DB 479 TLHLMAKAGLTLQOQHRLAQLLLILSHIRHMSKMGHEHLYSMKCKNVVPLYDLLLLL 538  
 QY 240 DAHRL 244  
 DB 539 DAHRL 543  
 RESULT 15  
 Q8CGK8 PRELIMINARY; PRT; 353 AA.  
 ID Q8CGK8;  
 AC Q8CGK8;  
 DT 01-MAR-2003 (TReMBLrel. 23, Created)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Estrogen receptor alpha (fragment).  
 GN Names=ESR1;  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2004, 08:14:27 ; Search time 11.951 Seconds  
(without alignments)  
1964.426 Million cell updates/sec

Title: US-09-830-693B-27  
Perfect score: 1250  
Sequence: 1 SLALS/TADQMSALLDAEP.....CKNVVPLYDLLLEMLDAHRL 244

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

To: Number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.79.\*

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1230.5	98.4	595	1 QRHUE	estrogen receptor
2	1204.5	96.4	599	1 QRMSE	estrogen receptor
3	1200.5	96.0	600	1 QRETE	estrogen receptor
4	1197.5	95.8	595	2 I47140	estradiol receptor
5	1177.5	94.2	701	2 S64737	80K estrogen recep
6	1176.5	94.1	589	1 QRCHE	estrogen receptor
7	1066.5	85.3	586	1 QRCHE	estrogen receptor
8	804.5	64.4	620	2 T10423	estrogen receptor
9	797.5	63.8	535	2 S58224	estrogen receptor
10	774.5	62.0	574	2 A37197	estrogen receptor
11	759.5	60.8	477	2 S71400	estrogen receptor
12	759.5	60.8	530	2 JC5939	estrogen receptor
13	746.5	59.7	503	2 JW0046	estrogen receptor
14	659.5	52.8	133	2 S26595	estrogen receptor
15	580.5	46.4	121	2 I67419	estradiol receptor
16	366.5	29.3	433	2 B29345	steroid hormone re
17	346.5	27.7	433	2 S58087	estrogen receptor
18	309	24.7	521	2 A29345	steroid hormone re
19	260.5	20.8	758	2 S60586	glucocorticoid rec
20	250	20.0	930	2 A25923	progesterone recep
21	249	19.9	933	1 QRHUP	progesterone recep
22	247.5	19.8	467	2 A43781	retinoid-X-recepto
23	246.5	19.7	786	2 A35466	retinoid-X-recepto
24	246	19.7	923	2 A39596	progesterone recep
25	245	19.6	923	2 I53280	progesterone recep
26	242	19.4	441	2 I50515	retinoid X recepto
27	240.5	19.2	488	2 C41977	retinoid receptor
28	238.5	19.1	463	2 S26670	retinoic acid rece
29	238.5	19.1	463	2 B41727	retinoid-X recepto

## ALIGNMENTS

## RESULT 1

## QRHUE

estrogen receptor 1 - human

N;Alternate names: ER1; estrogen receptor alpha

C;Species: Homo sapiens (man)

C;Date: 28-May-1986 #sequence revision 28-May-1986 #text change 09-Jul-2004

C;Accession: A94284; A93376; A43021; S27143; S34000; A41925; A03244; C41925; D41

R;Greene, G.L.; Gilna, P.; Waterfield, M.; Baker, A.; Hort, Y.; Shine, J.

Science 231, 1150-1154, 1986

A;Title: Sequence and expression of human estrogen receptor complementary DNA.

A;Reference number: A94284; MUID:86122927; PMID:3753802

A;Accession: A94284

A;Molecule type: mRNA

A;Residues: 1-595 <GR1>

A;Cross-references: UNIPROT:Q14268; UNIPROT:Q9UE35; GB:M12674; NID:g182192; PIDN:AAAS2339

R;Green, S.; Walker, P.; Kumar, V.; Krust, A.; Bornert, J.M.; Argos, P.; Chambon, P.

Nature 320, 134-139, 1986

A;Title: Human oestrogen receptor cDNA: sequence, expression and homology to v-erb-A.

A;Reference number: A93376; MUID:86146892; PMID:3754034

A;Accession: A93376

A;Molecule type: mRNA

A;Residues: 1-595 <GR2>

A;Cross-references: GB:X03635; NID:g31233; PIDN:CAA27284.1; PID:g31234

R;Ponglikitmongkol, M.; Green, S.; Chambon, P.

EMBO J. 7, 3385-3388, 1988

A;Title: Genomic organization of the human oestrogen receptor gene.

A;Reference number: A43021; MUID:89091079; PMID:3145193

A;Accession: A43021

A;Molecule type: DNA

A;Residues: 143-161;205-225;244-264;356-374,'G',376;402-422;447-460,'P',462-467;508-528

R;Keaveney, M.; Klug, J.; Gannon, F.

DNA Seq. 2, 347-358, 1992

A;Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene

A;Reference number: S27140; MUID:93075998; PMID:1476547

A;Accession: S27143

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-115 <KEA>

A;Cross-references: EMBL:X62462; NID:g31201; PIDN:CAA44322.1; PID:g31205

R;Pfeffer, U.; Fecarotta, B.; Castagnetta, L.; Vidali, G.

Cancer Res. 53, 741-743, 1993

A;Title: Estrogen receptor variant messenger RNA lacking exon 4 in estrogen-responsive h

A;Reference number: S34000; MUID:93153765; PMID:7916651

A;Accession: S34000

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 216-254,367-399,'G',401-434 <PFE>

A;Cross-references: EMBL:X73067; NID:g579865; PIDN:CAA51528.1; PID:g939886

A;Note: the authors translated the codon GGG for residue 400 as Val

R;Dotzlaw, H.; Alkhalaf, M.; Murphy, L.C.

Mol. Endocrinol. 6, 773-785, 1992

A;Title: Characterization of estrogen receptor variant mRNAs from human breast cancers.

A:Reference number: A41925; MUID:92293154; PMID:1603086  
A:Accession: A41925  
A:Molecule type: mRNA  
A:Residues: 1-214; 'ELPTLC' <DOT>  
A:Cross-references: GB:M69297; NID:g182218; PID:AAA58462.1; PID:g182219  
A:Experimental source: clone 4; breast cancer  
A:Note: the sequence has been revised after extraction from NCBI backbone  
A:Note: the complete sequence of neither the nucleotide nor the protein is shown in this  
A:Note: sequence extracted from NCBI backbone (NCBIN:106580)  
A:Accession: B41925  
A>Status: significant sequence differences  
A:Molecule type: mRNA  
A:Cross-references: GB:M69296  
A:Experimental source: clone 24; breast cancer  
A:Note: sequence extracted from NCBI backbone (NCBIN:106597)  
A:Comment: The steroid hormones and their receptors are involved in the regulation of eu  
C:Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly  
C:Comment: complex appears to recognize discrete DNA sequences upstream of transcriptional start site  
C:Genetics:  
A:Cross-references: GDB:119120; OMIM:133430  
A:Map position: 6q25.1-6q25.1  
A:Introns: 151/2; 215/1; 254/1; 366/1; 412/2; 457/1; 518/2  
C:Superfamily: estrogen receptor; erba transforming protein homology  
C:Keywords: DNA binding; nucleus; phosphoprotein; steroid hormone receptor; transcriptio  
F:1-120/Domain: amino-terminal <NH2>  
F:121-299/Domain: DNA binding #status predicted <DNA>  
F:183-456/Domain: erba transforming protein homology <ERBA>  
F:185-205/Region: zinc finger CCCC motif  
F:221-245/Region: zinc finger CCCC motif  
F:300-595/Domain: steroid binding #status predicted <STB>  
F:236,305/Binding site: phosphate (Ser) (covalent) #status predicted  
Query Match 98.4%; Score 1230.5; DB 1; Length 595;  
Best Local Similarity 99.2%; Pred. No. 1.3e-98;  
Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
QY 1 SLALSITADQVMSALLDAPPIYSEYDTPFPSEASMMGLLTNLADRELHMINWAKRV 60  
DB 305 SPALSITADQVMSALLDAPPIYSEYDTPFPSEASMMGLLTNLADRELHMINWAKRV 364  
QY 61 PGFVDLTLDQVHLLFCAMLEIMGLVWRSMEHPGKLLFAPNLLDRNQGKCVGWEI 120  
DB 365 PGFVDLTLDQVHLLFCAMLEIMGLVWRSMEHPGKLLFAPNLLDRNQGKCVGWEI 424  
QY 121 FDMLLATSSRFMMNLQGF-EFVCLKSIILLNSGVYTFLLSSTLKSLEEKDHIHRVLDKITD 179  
DB 425 FDMLLATSSRFMMNLQGF-EFVCLKSIILLNSGVYTFLLSSTLKSLEEKDHIHRVLDKITD 484  
QY 180 TLHLMMAKGLTLQOQHRLAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPYDLLLLLEML 239  
DB 485 TLHLMMAKGLTLQOQHRLAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPYDLLLLLEML 544  
QY 240 DAHRL 244  
DB 545 DAHRL 549  
RESULT 2  
ORFSE  
estrogen receptor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 06-Mar-1992 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004  
C:Accession: A40061  
R:White, R.; Lees, J.A.; Needham, M.; Ham, J.; Parker, M.  
Mol. Endocrinol. 1, 735-744, 1987  
A:Title: Structural organization and expression of the mouse estrogen receptor.  
A:Reference number: A40061; MUID:91042558; PMID:2484714  
A:Accession: A40061  
A:Molecule type: mRNA  
A:Residues: 1-599 <WHI>  
A:Cross-references: UNIPROT:P19785; GB:M38651; NID:g193179; PID:AAA37580.1; PID:g193180  
C:Comment: The steroid hormones and their receptors are involved in the regulation of eu

C:Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly  
C:Comment: complex appears to recognize discrete DNA sequences upstream of transcriptional start site  
C:Superfamily: estrogen receptor; erba transforming protein homology  
C:Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recept  
F:1-183/Domain: amino-terminal <NH2>  
F:184-275/Domain: DNA binding #status predicted <DNA>  
F:187-460/Domain: erba transforming protein homology <ERBA>  
F:187-210/Region: zinc finger CCCC motif  
F:223-245/Region: zinc finger CCCC motif  
F:260-275/Region: nuclear location signal  
F:304-556/Domain: steroid binding #status predicted <STB>  
F:189,192,206,209/Binding site: zinc (Cys) #status predicted  
F:225,231,241,244/Binding site: zinc (Cys) #status predicted  
F:240,309/Binding site: phosphate (Ser) (covalent) #status predicted  
Query Match 96.4%; Score 1204.5; DB 1; Length 599;  
Best Local Similarity 96.3%; Pred. No. 2.4e-96;  
Matches 236; Conservative 5; Mismatches 3; Indels 1; Gaps 1;  
QY 1 SLALSITADQVMSALLDAPPIYSEYDTPFPSEASMMGLLTNLADRELHMINWAKRV 60  
DB 309 SPALSITADQVMSALLDAPPIYSEYDTPFPSEASMMGLLTNLADRELHMINWAKRV 368  
QY 61 PGFVDLTLDQVHLLFCAMLEIMGLVWRSMEHPGKLLFAPNLLDRNQGKCVGWEI 120  
DB 369 PGFVDLTLDQVHLLFCAMLEIMGLVWRSMEHPGKLLFAPNLLDRNQGKCVGWEI 428  
QY 121 FDMLLATSSRFMMNLQGF-EFVCLKSIILLNSGVYTFLLSSTLKSLEEKDHIHRVLDKITD 179  
DB 429 FDMLLATSSRFMMNLQGF-EFVCLKSIILLNSGVYTFLLSSTLKSLEEKDHIHRVLDKITD 488  
QY 180 TLHLMMAKGLTLQOQHRLAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPYDLLLLLEML 239  
DB 489 TLHLMMAKGLTLQOQHRLAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPYDLLLLLEML 548  
QY 240 DAHRL 244  
DB 549 DAHRL 553  
RESULT 3  
ORFTE  
estrogen receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Sep-1991 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004  
C:Accession: S07379; S16731  
R:Koike, S.; Sakai, M.; Muramatsu, M.  
Nucleic Acids Res. 15, 2499-2513, 1987  
A:Title: Molecular cloning and characterization of rat estrogen receptor cDNA.  
A:Reference number: S07379; MUID:87174780; PMID:3031601  
A:Accession: S07379  
A:Molecule type: mRNA  
A:Residues: 1-600 <KOI>  
A:Cross-references: UNIPROT:P06211; EMBL:X00102; NID:g56110; PID:CAA68287.1; PID:g56111  
R:Maggi, A.M.A.  
submitted to the EMBL Data Library, June 1991  
A:Reference number: S16731  
A:Accession: S16731  
A:Molecule type: mRNA  
A:Residues: 1-487; 'T', 489-600 <MAG>  
A:Cross-references: EMBL:X61098; NID:g56120; PID:CAA43411.1; PID:g56121  
C:Comment: The steroid hormones and their receptors are involved in the regulation of eu  
C:Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly  
C:Comment: complex appears to recognize discrete DNA sequences upstream of transcriptional start site  
C:Superfamily: estrogen receptor; erba transforming protein homology  
C:Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recept  
F:1-184/Domain: amino-terminal <NH2>  
F:185-276/Domain: DNA binding #status predicted <DNA>  
F:188-461/Domain: erba transforming protein homology <ERBA>  
F:188-211/Region: zinc finger CCCC motif  
F:224-246/Region: zinc finger CCCC motif  
F:261-276/Region: nuclear location signal  
F:305-557/Domain: steroid binding #status predicted <STB>

F;190,193,207,210/Binding site: zinc (Cys) #status predicted  
F;242,232,242,245/Binding site: zinc (Cys) #status predicted  
F;241,310/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 96.0%; Score 1200.5; DB 1; Length 600;  
Best Local Similarity 95.9%; Pred. No. 5.3e-96;  
Matches 235; Conservative 5; Mismatches 4; Indels 1; Gaps 1;  
Qy 1 SLALSLTADQVMSALLDAEPPIIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
Db 310 SPALSLTADQVMSALLDAEPPIIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 369  
Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQCCKVEGVMEI 120  
Db 370 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQCCKVEGVMEI 429  
Qy 121 FDMLLATSSFRMNNLQGEFVCLKSIILLNSGVYTFSLSTLSLEKDHHRVLDKTD 179  
Db 430 FDMLLATSSFRMNNLQGEFVCLKSIILLNSGVYTFSLSTLSLEKDHHRVLDKTD 489  
Qy 180 TLHLMAKAGITLQOQHRLAQLLLILSHIRHNSKGMHEHLYSMKCKNVVPLDYLLLEML 239  
Db 490 TLHLMAKAGITLQOQHRLAQLLLILSHIRHNSKGMHEHLYSMKCKNVVPLDYLLLEML 549  
Qy 240 DAHRL 244  
Db 550 DAHRL 554

RESULT 4  
147140  
estradriol receptor - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 21-Feb-1997 #sequence revision 21-Feb-1997 #text\_change 09-Jul-2004  
C;Accession: 147140; S66250; S32402  
R;Bokenkamp, D.; Jungblut, P.W.; Thole, H.H.  
Mol. Cell. Endocrinol. 104, 163-172, 1994  
A;Title: The C-terminal half of the porcine estradiol receptor contains no post-translational modification  
A;Reference number: 147140; MUID:95080454; PMID:7988744  
A;Accession: 147140  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-595 <BOK>  
A;Cross-references: UNIPROT:Q23040; EMBL:Z37167; NID:9587554; PID:9587554  
A;Experimental source: uterus  
R;Thole, H.H.; Maschler, I.; Jungblut, P.W.  
Eur. J. Biochem. 231, 510-516, 1995  
A;Title: Surface mapping of the ligand-filled C-terminal half of the porcine estradiol receptor  
A;Reference number: S66250; MUID:95361877; PMID:7635163  
A;Accession: S66250  
A;Molecule type: protein  
A;Residues: 297-307;310-313;320-323;329-332;337-340;417-420;466-473 <THO>  
R;Thole, H.H.  
FEBS Lett. 320, 92-96, 1993  
A;Title: Assignment of the ligand binding site of the porcine estradiol receptor to the C-terminal half of the receptor  
A;Reference number: S32402; MUID:93209384; PMID:8458437  
A;Accession: S32402  
A;Molecule type: protein  
A;Residues: 303-323 <THW>  
C;Superfamily: estrogen receptor; erba transforming protein homology  
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid hormone receptor; transactivator  
F;120/Domain: amino-terminal <NH2>  
F;121-299/Domain: DNA binding #status predicted <DNA>  
F;183-456/Domain: erba transforming protein homology <ERBA>  
F;185-205/Region: zinc finger CCCC motif  
F;221-245/Region: zinc finger CCCC motif  
F;256-271/Region: nuclear location signal  
F;300-595/Domain: steroid binding #status predicted <STB>  
F;185,188,202,205/Binding site: zinc (Cys) #status predicted  
F;221,227,237,240/Binding site: zinc (Cys) #status predicted  
F;236,305/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 95.8%; Score 1197.5; DB 2; Length 595;  
Best Local Similarity 95.1%; Pred. No. 9.5e-96;  
Matches 233; Conservative 7; Mismatches 4; Indels 1; Gaps 1;  
Qy 1 SLALSLTADQVMSALLDAEPPIIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
Db 305 SPVLSTADQVMSALLDAEPPIIYSEYDTPRPLSEASMMGLLTNLADRELVHMINWAKRV 364  
Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQCCKVEGVMEI 120  
Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQCCKVEGVMEI 424  
Qy 121 FDMLLATSSFRMNNLQGEFVCLKSIILLNSGVYTFSLSTLSLEKDHHRVLDKTD 179  
Db 425 FDMLLATSSFRMNNLQGEFVCLKSIILLNSGVYTFSLSTLSLEKDHHRVLDKTD 484  
Qy 180 TLHLMAKAGITLQOQHRLAQLLLILSHIRHNSKGMHEHLYSMKCKNVVPLDYLLLEML 239  
Db 485 TLHLMAKAGITLQOQHRLAQLLLILSHIRHNSKGMHEHLYSMKCKNVVPLDYLLLEML 544  
Qy 240 DAHRL 244  
Db 545 DAHRL 549

RESULT 5  
S64737  
80K estrogen receptor - human  
C;Species: Homo sapiens (man)  
C;Date: 28-Oct-1996 #sequence revision 13-Mar-1997 #text\_change 20-Aug-1999  
C;Accession: S64737  
R;Pink, J.J.; Wu, S.Q.; Wolf, D.M.; Billimoria, M.M.; Jordan, V.C.  
Nucleic Acids Res. 24, 962-969, 1996  
A;Title: A novel 80 kDa human estrogen receptor containing a duplication of exons 6 and 7  
A;Reference number: S64737; MUID:96174665; PMID:8600466  
A;Accession: S64737  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-701 <PIN>  
A;Cross-references: EMBL:U47678; NID:96174665; PID:96174665  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996  
C;Superfamily: estrogen receptor; erba transforming protein homology  
C;Keywords: steroid hormone receptor; zinc finger  
F;183-456/Domain: erba transforming protein homology <ERBA>  
F;518-562/Domain: erba transforming protein homology #status atypical <ERB2>

Query Match 94.2%; Score 1177.5; DB 2; Length 701;  
Best Local Similarity 69.2%; Pred. No. 6.3e-94;  
Matches 243; Conservative 0; Mismatches 1; Indels 107; Gaps 1;  
Qy 1 SLALSLTADQVMSALLDAEPPIIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
Db 305 SLALSLTADQVMSALLDAEPPIIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364  
Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQCCKVEGVMEI 120  
Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQCCKVEGVMEI 424  
Qy 121 FDMLLATSSFRMNNLQGEFVCLKSIILLNSGVYTFSLSTLSLEKDHHRVLDKTD 138  
Db 425 FDMLLATSSFRMNNLQGEFVCLKSIILLNSGVYTFSLSTLSLEKDHHRVLDKTD 484  
Qy 139 -----  
Db 485 TLHLMAKAGITLQOQHRLAQLLLILSHIRHNSKGMHEHLYSMKCKNVVPLDYLLLEML 544  
Qy 139 -----EFVCLKSIILLNSGVYTFSLSTLSLEKDHHRVLDKTDTLHLMAKAGITLQ 193  
Db 545 NLOGSEFVCLKSIILLNSGVYTFSLSTLSLEKDHHRVLDKTDTLHLMAKAGITLQ 604  
Qy 194 QQHRLAQLLLILSHIRHNSKGMHEHLYSMKCKNVVPLDYLLLEMLDAHRL 244  
Db 605 QQHRLAQLLLILSHIRHNSKGMHEHLYSMKCKNVVPLDYLLLEMLDAHRL 655

## RESULT 6

QRCHE

estrogen receptor - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 06-Mar-1992 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004  
C:Accession: A40914; S07192  
R:Maxwell, B.L.; McDonnell, D.P.; Conneely, O.M.; Schulz, T.Z.; Greene, G.L.; O'Malley, M.J. Endocrinol. 1, 25-35, 1987  
A:Title: Structural organization and regulation of the chicken estrogen receptor.  
A:Reference number: A40914; MUID:88318621; PMID:2901032  
A:Accession: A40914

A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-589 <MAX>  
A:Cross-References: UNIPROT:P06212  
R:Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P. EMBO J. 5, 891-897, 1986  
A:Comment: The chicken estrogen receptor sequence: homology with v-erbA and the human oes  
A:Reference number: S07192; MUID:86247578; PMID:3755102  
A:Accession: S07192  
A:Status: preliminary  
A:Molecule type: mRNA

A:Residues: 1-256, 'E' 258-589 <KRU>  
A:Cross-References: EMBL:X03805; NID:G63378; PIDN:CAA27433.1; PID:G63380  
C:Comment: The steroid hormones and their receptors are involved in the regulation of eu  
C:Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly  
complex appears to recognize discrete DNA sequences upstream of transcriptional start sit  
C:Superfamily: estrogen receptor; erbA transforming protein homology  
C:Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep  
F:1-173/Domain: amino-terminal <NH2>  
F:174-265/Domain: DNA binding #status predicted <DNA>  
F:177-450/Domain: erbA transforming protein homology <ERBA>  
F:177-200/Region: zinc finger CCCC motif  
F:213-235/Region: zinc finger CCCC motif  
F:250-265/Region: nuclear location signal  
F:294-546/Domain: steroid binding #status predicted <STB>  
F:179,182,196,199/Binding site: zinc (Cys) #status predicted  
F:215,221,231,234/Binding site: zinc (Cys) #status predicted  
F:230,299/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 94.1%; Score 1176.5; DB 1; Length 589;  
Best Local Similarity 93.5%; Pred. No. 6.2e-94; Mismatches 3; Indels 1; Gaps 1;  
Matches 229; Conservative 12;

QY 1 SLALSITADQVMSALLDAPPIYSEYDTPRPFSEASMMGLTTLNADRELVHMINWAKRV 60  
Db 299 SPALSITAEQVMSALLEAPPIYSEYDTPRPFSEASMMGLTTLNADRELVHMINWAKRV 358

QY 61 PGFVDLTLDQVHLLCAWLEIMGLVWRSMEHPGKLLFAPNLLDRNQKCVGVMVEI 120  
Db 359 PGFVDLTLDQVHLLCAWLEIMGLVWRSMEHPGKLLFAPNLLDRNQKCVGVMVEI 418

QY 121 FDMLLATSSRFPMNLQGEFVCLSKSIILNSGVVTFSLSTLSKEEDHHRVLDKIID 179  
Db 419 FDMLLATSSRFPMNLQGEFVCLSKSIILNSGVVTFSLSTLSKEEDHHRVLDKIID 478

QY 180 TLHLMAKAGLTQQOQHRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPYDYLLEML 239  
Db 479 TLHLMAKAGLTQQOQHRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPYDYLLEML 538

QY 240 DAHRL 244  
Db 539 DAHRL 543

## RESULT 7

QRCHE

estrogen receptor - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 28-Feb-1992 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004  
C:Accession: A40907

R&gt;Weiler, J.J.; Lew, D.; Shapiro, D.J.

Mol. Endocrinol. 1, 355-362, 1987

A:Title: The Xenopus laevis estrogen receptor: sequence homology with human and avian rec  
A:Reference number: A40907; MUID:90331927; PMID:3274894  
A:Accession: A40907

A:Molecule type: mRNA

A:Residues: 1-586 &lt;WEI&gt;

A:Cross-References: UNIPROT:P81559; GB:I20735

C:Comment: The steroid hormones and their receptors are involved in the regulation of eu  
C:Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly  
complex appears to recognize discrete DNA sequences upstream of transcriptional start sit  
C:Superfamily: estrogen receptor; erbA transforming protein homology  
C:Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep  
F:1-174/Domain: amino-terminal <NH2>  
F:175-266/Domain: DNA binding #status predicted <DNA>  
F:178-448/Domain: erbA transforming protein homology <ERBA>  
F:214-237/Region: zinc finger CCCC motif  
F:251-266/Region: nuclear location signal  
F:292-544/Domain: steroid binding #status predicted <STB>  
F:180,183,197,200/Binding site: zinc (Cys) #status predicted  
F:216,222,232,235/Binding site: zinc (Cys) #status predicted  
F:231/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 85.3%; Score 1066.5; DB 1; Length 586;  
Best Local Similarity 82.9%; Pred. No. 2e-84; Mismatches 26; Indels 1; Gaps 1;  
Matches 203; Conservative 26;

QY 1 SLALSITADQVMSALLDAPPIYSEYDTPRPFSEASMMGLTTLNADRELVHMINWAKRV 60  
Db 297 SPVLSITAEQLISALMEAPPIYSEHSTKPLSEASMMGLTTLNADRELVHMINWAKRV 356

QY 61 PGFVDLTLDQVHLLCAWLEIMGLVWRSMEHPGKLLFAPNLLDRNQKCVGVMVEI 120  
Db 357 PGFVDLTLDQVHLLCAWLEIMGLVWRSMEHPGKLLFAPNLLDRNQKCVGVMVEI 416

QY 121 FDMLLATSSRFPMNLQGEFVCLSKSIILNSGVVTFSLSTLSKEEDHHRVLDKIID 179  
Db 417 FDMLLATSSRFPMNLQGEFVCLSKSIILNSGVVTFSLSTLSKEEDHHRVLDKIID 476

QY 180 TLHLMAKAGLTQQOQHRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPYDYLLEML 239  
Db 477 TLVHFMKAGLTQQOQHRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPYDYLLEML 536

QY 240 DAHRL 244  
Db 537 DAHRI 541

## RESULT 8

T10423

estrogen receptor - Oryzias sp. (strain d-rR)

C:Species: Oryzias sp.

A:Variety: strain d-rR

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C:Accession: T10423

R:Okada, H.; Kawahara, T.; Yamashita, I.

submitted to the EMBL Data Library, March 1994

A:Description: Cloning of medaka estrogen receptor cDNA.

A:Reference number: Z17013

A:Accession: T10423

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-620 &lt;OKA&gt;

A:Cross-References: UNIPROT:P50241; EMBL:D28954

A:Experimental source: strain d-rR, liver

C:Genetics: MER

C:Superfamily: estrogen receptor; erbA transforming protein homology

C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation

F:184-460/Domain: erbA transforming protein homology &lt;ERB&gt;

Query Match 64.4%; Score 804.5; DB 2; Length 620;







C:Species: Macaca mulatta (rhesus macaque)  
 C:Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 09-Jul-2004  
 C:Accession: I67419  
 R:Chandrasekhar, Y.A.; Melner, M.H.; Nagalla, S.R.; Stouffer, R.L.  
 Endocrinology 135, 307-314, 1994  
 A:Title: Progesterone receptor, but not estradiol receptor, messenger ribonucleic acid  
 A:Reference number: 153287; MUID:94283272; PMID:8013365  
 A:Accession: I67419  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-121 <RES>  
 A:Cross-references: UNIPROT:P49886; GB:S71040; NID:G547182; PIDN:AA831102.1; PID:G547183  
 C:Superfamily: estrogen receptor; erba transforming protein homology  
 C:Keywords: steroid hormone receptor; zinc finger  
 F:1-54/Domain: erba transforming protein homology (fragment) <ERBA>

Query Match 46.4%; Score 580.5; DB 2; Length 121;  
 Best Local Similarity 97.5%; Pred. No. 3.2e-43;  
 Matches 118; Conservative 1; Mismatches 1; Indels 1; Gaps 1;  
 Qy 99 LFAPNLLDRNQKCGVEGMVEIFDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF 157  
 Db 1 LFAPNLLDRNQKCGVEGMVEIFDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF 60  
 Qy 158 SSTLSLEEKDHIHRVLDKITDTLIHLMAKAGLTQQOHRRLAQQLLILSHIRHMSNKG 217  
 Db 61 SSTLSLEEKDHIHRVLDKITDTLIHLMAKAGLTQQOHRRLAQQLLILSHIRHMSNKG 120  
 Qy 218 E 218  
 Db 121 E 121

Search completed: November 8, 2004, 08:28:28  
 Job time : 12.951 secs

*This Page Blank (uspto)*

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2004, 08:28:04 ; Search time 36.849 Seconds  
(without alignments)  
2338.928 Million cell updates/sec

Title: US-09-830-693B-27

Perfect score: 1250

Sequence: 1 SLALSUTADQMSALLDAEP.....CKNVPLYDLLEMLDAHRL 244

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

To: number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1239.5	99.2	414	14	US-10-157-899A-2
2	1239.5	99.2	438	14	US-10-157-899A-4
3	1239.5	99.2	595	14	US-09-853-033-2
4	1239.5	99.2	595	14	US-10-148-835-1
5	1239.5	99.2	595	14	US-10-148-835-2
6	1239.5	99.2	595	14	US-10-148-835-9
7	1239.5	98.8	595	14	US-10-148-835-5
8	1233.5	98.7	595	14	US-10-148-835-3
9	1232.5	98.6	595	14	US-10-148-835-4
10	1232.5	98.6	595	14	US-10-148-835-10
11	1231.5	98.5	595	14	US-10-148-835-8
12	1231.5	98.5	660	9	US-09-853-033-4
13	1230.5	98.4	414	14	US-10-157-899A-8

14	1230.5	98.4	438	14	US-10-157-899A-14
15	1230.5	98.4	511	14	US-10-006-760-19
16	1230.5	98.4	547	14	US-10-052-092-10
17	1230.5	98.4	547	14	US-10-437-107-10
18	1230.5	98.4	591	14	US-10-278-481-17
19	1230.5	98.4	595	9	US-09-933-267A-2
20	1230.5	98.4	595	10	US-09-952-680A-10
21	1230.5	98.4	595	13	US-10-096-710-1
22	1230.5	98.4	595	13	US-10-081-563-2
23	1230.5	98.4	595	14	US-10-052-092-9
24	1230.5	98.4	595	14	US-10-052-092-13
25	1230.5	98.4	595	14	US-10-052-092-14
26	1230.5	98.4	595	14	US-10-207-655-61
27	1230.5	98.4	595	14	US-10-177-293-128
28	1230.5	98.4	595	14	US-10-157-899A-55
29	1230.5	98.4	595	14	US-10-437-107-9
30	1230.5	98.4	595	14	US-10-437-107-13
31	1230.5	98.4	595	14	US-10-437-107-14
32	1230.5	98.4	595	14	US-10-095-373A-2
33	1230.5	98.4	595	14	US-10-392-274-2
34	1230.5	98.4	595	14	US-10-148-835-6
35	1230.5	98.4	595	14	US-10-148-835-7
36	1230.5	98.4	595	14	US-10-144-198-42
37	1230.5	98.4	676	14	US-10-095-373A-73
38	1230.5	98.4	677	14	US-10-095-373A-69
39	1230.5	98.4	726	14	US-10-095-373A-71
40	1230.5	98.4	727	14	US-10-095-373A-67
41	1229.5	98.4	414	14	US-10-157-899A-10
42	1229.5	98.4	438	14	US-10-157-899A-16
43	1228.5	98.3	660	9	US-09-853-033-8
44	1227.5	98.2	242	15	US-10-355-218-10
45	1225.5	98.0	414	14	US-10-157-899A-6

## ALIGNMENTS

### RESULT 1

US-10-157-899A-2

; Sequence 2, Application US/10157899A  
; Publication No. US20030143559A1  
; GENERAL INFORMATION:  
; APPLICANT: Bracken, Kathryn Rene  
; APPLICANT: de los Angeles, Joseph Ernest  
; APPLICANT: Huang, Ying  
; APPLICANT: Kadan, Michael Joseph  
; APPLICANT: Keander, Gary Michael  
; APPLICANT: Zerby, Dennis  
; TITLE OF INVENTION: NOVEL ESTROGEN RECEPTOR LIGAND BINDING DOMAIN VARIANTS AND NOVEL  
; FILE REFERENCE: 4-32018A  
; CURRENT APPLICATION NUMBER: US/10/157,899A  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 60/294,839  
; PRIOR FILING DATE: 2001-05-31  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 414  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fusion of the human-Estrogen-receptor-ligand-binding-domain and a  
; OTHER INFORMATION: zinc finger array (C7)  
US-10-157-899A-2

Query Match 99.2%; Score 1239.5; DB 14; Length 414;

Best Local Similarity 99.6%; Pred. No. 2e-118;

Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SLALSUTADQMSALLDAEPILYSEYDPTPTPSEASMGGLTTLADRELVHMINAKRV 60

Db 122 SLALSUTADQMSALLDAEPILYSEYDPTPTPSEASMGGLTTLADRELVHMINAKRV 181

QY 61 PGFVDLTLDQVHLLCAWLEITLMTGLVWRSMEHPGKLLFAPNLLLDNRQKCVGWEI 120  
DB 182 PGFVDLTLDQVHLLCAWLEITLMTGLVWRSMEHPGKLLFAPNLLLDNRQKCVGWEI 241  
QY 121 FOMLATSSRFMMNLQGEFFVCLSKSIIILLNSGVVTFSLSTLSLEEKDHIHRVLDKTD 179  
DB 242 FOMLATSSRFMMNLQGEFFVCLSKSIIILLNSGVVTFSLSTLSLEEKDHIHRVLDKTD 301  
QY 180 TLIIHMAKAGLTLOQOQHRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPYDYLLEML 239  
DB 302 TLIIHMAKAGLTLOQOQHRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPYDYLLEML 361  
QY 240 DAHRL 244  
DB 362 DAHRL 366

RESULT 2  
US-157-899A-4  
; Sequence 4, Application US/10157899A  
; Patent No. US20030143559A1  
; GENERAL INFORMATION:  
; APPLICANT: Bracken, Kathryn Rene  
; APPLICANT: Huang, Ying  
; APPLICANT: Kadan, Michael Joseph  
; APPLICANT: Keander, Gary Michael  
; APPLICANT: Zerby, Dennis  
; TITLE OF INVENTION: NOVEL ESTROGEN RECEPTOR LIGAND BINDING DOMAIN VARIANTS AND NOVEL  
; FILE REFERENCE: 4-32018A  
; CURRENT APPLICATION NUMBER: US/10/157,899A  
; PRIOR FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 60/294,839  
; PRIOR FILING DATE: 2001-05-31  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 438  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fusion of the human-Estrogen-receptor-ligand-binding-domain and a  
; OTHER INFORMATION: zinc finger array (C7)  
US-10-157-899A-4

Query Match 99.2%; Score 1239.5; DB 14; Length 438;  
Best Local Similarity 99.6%; Pred. No. 2.1e-118;  
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 SLALSLTADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 146 SLALSLTADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 205  
QY 61 PGFVDLTLDQVHLLCAWLEITLMTGLVWRSMEHPGKLLFAPNLLLDNRQKCVGWEI 120  
DB 206 PGFVDLTLDQVHLLCAWLEITLMTGLVWRSMEHPGKLLFAPNLLLDNRQKCVGWEI 265  
QY 121 FOMLATSSRFMMNLQGEFFVCLSKSIIILLNSGVVTFSLSTLSLEEKDHIHRVLDKTD 179  
DB 266 FOMLATSSRFMMNLQGEFFVCLSKSIIILLNSGVVTFSLSTLSLEEKDHIHRVLDKTD 325  
QY 180 TLIIHMAKAGLTLOQOQHRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPYDYLLEML 239  
DB 326 TLIIHMAKAGLTLOQOQHRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPYDYLLEML 385  
QY 240 DAHRL 244  
DB 386 DAHRL 390

RESULT 3

US-09-853-033-2  
; Sequence 2, Application US/09853033  
; Patent No. US20020100068A1  
; GENERAL INFORMATION:  
; APPLICANT: CHAMBERON, PIERRE  
; APPLICANT: METZGER, DANIEL  
; TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION  
; FILE REFERENCE: 065691/0222  
; CURRENT APPLICATION NUMBER: US/09/853,033  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: FR 00/12570  
; PRIOR FILING DATE: 2000-10-03  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 595  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-853-033-2

Query Match 99.2%; Score 1239.5; DB 9; Length 595;  
Best Local Similarity 99.6%; Pred. No. 3.2e-118;  
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 SLALSLTADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 305 SLALSLTADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364  
QY 61 PGFVDLTLDQVHLLCAWLEITLMTGLVWRSMEHPGKLLFAPNLLLDNRQKCVGWEI 120  
DB 365 PGFVDLTLDQVHLLCAWLEITLMTGLVWRSMEHPGKLLFAPNLLLDNRQKCVGWEI 424  
QY 121 FOMLATSSRFMMNLQGEFFVCLSKSIIILLNSGVVTFSLSTLSLEEKDHIHRVLDKTD 179  
DB 425 FOMLATSSRFMMNLQGEFFVCLSKSIIILLNSGVVTFSLSTLSLEEKDHIHRVLDKTD 484  
QY 180 TLIIHMAKAGLTLOQOQHRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPYDYLLEML 239  
DB 485 TLIIHMAKAGLTLOQOQHRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPYDYLLEML 544  
QY 240 DAHRL 244  
DB 545 DAHRL 549

RESULT 4  
US-10-148-835-1  
; Sequence 1, Application US/10148835  
; Publication No. US20030207380A1  
; GENERAL INFORMATION:  
; APPLICANT: SAITO et al.  
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION  
; FILE REFERENCE: 2185-0648P  
; CURRENT APPLICATION NUMBER: US/10/148,835  
; CURRENT FILING DATE: 2002-10-11  
; NUMBER OF SEQ ID NOS: 213  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 595  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-148-835-1

Query Match 99.2%; Score 1239.5; DB 14; Length 595;  
Best Local Similarity 99.6%; Pred. No. 3.2e-118;  
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 SLALSLTADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 305 SLALSLTADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364  
QY 61 PGFVDLTLDQVHLLCAWLEITLMTGLVWRSMEHPGKLLFAPNLLLDNRQKCVGWEI 120

```

Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 424
Qy 121 FDMLLATSSRFMMNLOG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHHRVLDKITD 179
Db 425 FDMLLATSSRFMMNLOGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHHRVLDKITD 484
Qy 180 TLIHMAKAGITLQOQHRLAQLLLILSHIRHMSKGMHEHLYSMKCKNVVPLYDILLEML 239
Db 485 TLIHMAKAGITLQOQHRLAQLLLILSHIRHMSKGMHEHLYSMKCKNVVPLYDILLEML 544
Qy 240 DAHRL 244
Db 545 DAHRL 549

```

```

RESULT 5
US-10-148-835-2
; Sequence 2, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-2

```

```

Query Match 99.2%; Score 1239.5; DB 14; Length 595;
Best Local Similarity 99.6%; Pred. No. 3.2e-118;
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SLALSTADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSTADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120
Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 424
Qy 121 FDMLLATSSRFMMNLOG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHHRVLDKITD 179
Db 425 FDMLLATSSRFMMNLOGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHHRVLDKITD 484
Qy 180 TLIHMAKAGITLQOQHRLAQLLLILSHIRHMSKGMHEHLYSMKCKNVVPLYDILLEML 239
Db 485 TLIHMAKAGITLQOQHRLAQLLLILSHIRHMSKGMHEHLYSMKCKNVVPLYDILLEML 544
Qy 240 DAHRL 244
Db 545 DAHRL 549

```

```

RESULT 6
US-10-148-835-9
; Sequence 9, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 595

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-9

Query Match 99.2%; Score 1239.5; DB 14; Length 595;
Best Local Similarity 99.6%; Pred. No. 3.2e-118;
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SLALSTADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSTADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120
Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 424
Qy 121 FDMLLATSSRFMMNLOG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHHRVLDKITD 179
Db 425 FDMLLATSSRFMMNLOGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHHRVLDKITD 484
Qy 180 TLIHMAKAGITLQOQHRLAQLLLILSHIRHMSKGMHEHLYSMKCKNVVPLYDILLEML 239
Db 485 TLIHMAKAGITLQOQHRLAQLLLILSHIRHMSKGMHEHLYSMKCKNVVPLYDILLEML 544
Qy 240 DAHRL 244
Db 545 DAHRL 549

```

```

RESULT 7
US-10-148-835-5
; Sequence 5, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-5

```

```

Query Match 98.8%; Score 1235.5; DB 14; Length 595;
Best Local Similarity 99.2%; Pred. No. 8.3e-118;
Matches 243; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SLALSTADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSTADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120
Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 424
Qy 121 FDMLLATSSRFMMNLOG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHHRVLDKITD 179
Db 425 FDMLLATSSRFMMNLOGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHHRVLDKITD 484
Qy 180 TLIHMAKAGITLQOQHRLAQLLLILSHIRHMSKGMHEHLYSMKCKNVVPLYDILLEML 239
Db 485 TLIHMAKAGITLQOQHRLAQLLLILSHIRHMSKGMHEHLYSMKCKNVVPLYDILLEML 544
Qy 240 DAHRL 244
Db 545 DAHRL 549

```

RESULT 8

```
US-10-148-835-3
; Sequence 3, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-3

Query Match      98.7%; Score 1232.5; DB 14; Length 595;
Best Local Similarity 99.2%; Pred. No. 1.3e-117;
Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
    |||||
Db 305 SLALFLTADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
    |||||
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 120
    |||||
Db 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 424
    |||||
QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLSEKDHHRVLDKIDT 179
    |||||
Db 425 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLSEKDHHRVLDKIDT 484
    |||||
QY 180 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 239
    |||||
Db 485 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 544
    |||||
QY 240 DAHRL 244
    |||||
Db 545 DAHRL 549
    |||||

RESULT 9
US-10-148-835-4
; Sequence 4, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-4

Query Match      98.6%; Score 1232.5; DB 14; Length 595;
Best Local Similarity 99.2%; Pred. No. 1.7e-117;
Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
    |||||
Db 305 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
    |||||
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 120
    |||||
Db 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 424
    |||||
QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLSEKDHHRVLDKIDT 179
    |||||
Db 425 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLSEKDHHRVLDKIDT 484
    |||||
QY 180 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 239
    |||||
Db 485 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 544
    |||||
QY 240 DAHRL 244
    |||||
Db 545 DAHRL 549
    |||||

RESULT 11
US-10-148-835-8
; Sequence 8, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-8

Query Match      98.6%; Score 1232.5; DB 14; Length 595;
Best Local Similarity 99.2%; Pred. No. 1.7e-117;
Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
    |||||
Db 305 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
    |||||
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 120
    |||||
Db 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 424
    |||||
QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLSEKDHHRVLDKIDT 179
    |||||
Db 425 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLSEKDHHRVLDKIDT 484
    |||||
QY 180 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 239
    |||||
Db 485 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 544
    |||||
QY 240 DAHRL 244
    |||||
Db 545 DAHRL 549
    |||||

RESULT 11
US-10-148-835-10
; Sequence 10, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-10

Query Match      98.6%; Score 1232.5; DB 14; Length 595;
Best Local Similarity 99.2%; Pred. No. 1.7e-117;
Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
    |||||
Db 305 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
    |||||
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 120
    |||||
Db 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 424
    |||||
QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLSEKDHHRVLDKIDT 179
    |||||
Db 425 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLSEKDHHRVLDKIDT 484
    |||||
QY 180 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 239
    |||||
Db 485 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 544
    |||||
QY 240 DAHRL 244
    |||||
Db 545 DAHRL 549
    |||||

RESULT 10
US-10-148-835-10
; Sequence 10, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-10

Query Match      98.6%; Score 1232.5; DB 14; Length 595;
Best Local Similarity 99.2%; Pred. No. 1.7e-117;
Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
    |||||
Db 305 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
    |||||
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 120
    |||||
Db 365 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 424
    |||||
QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLSEKDHHRVLDKIDT 179
    |||||
Db 425 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLSEKDHHRVLDKIDT 484
    |||||
QY 180 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 239
    |||||
Db 485 TLIHLMKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLEML 544
    |||||
QY 240 DAHRL 244
    |||||
Db 545 DAHRL 549
    |||||
```



Query Match 98.5%; Score 1231.5; DB 14; Length 595;  
Best Local Similarity 98.8%; Pred. No. 2.1e-117;  
Matches 242; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 1 SLALSLTADQVMSALLDAEPPILYSEYDPTPTFSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 305 SLALSLTADQVMSALLDAEPPILYSEYDPTPTFSEASMMGLLTNLADRELVHMINWAKRV 364  
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGVEI 120  
DB 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGVEI 424  
QY 121 FDMLLATSSFRMNNLQGEFVCLKSIILLNSGYVTFSLSTLKSLEKDHHRVLDKITD 179  
DB 425 FDMLLATSSFRMNNLQGEFVCLKSIILLNSGYVTFSLSTLKSLEKDHHRVLDKITD 484  
QY 180 TLHLMAKAGLTQQQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 239  
DB 485 TLHLMAKAGLTQQQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 544  
QY 240 DAHRL 244  
DB 545 DAHRL 549

RESULT 12  
US-09-853-033-4  
; Sequence 4, Application US/09853033  
; Patent No. US2002010068A1  
; GENERAL INFORMATION:  
; APPLICANT: CHAMBERON, PIERRE  
; APPLICANT: METZGER, DANIEL  
; TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION  
; FILE REFERENCE: 065691/0222  
; CURRENT APPLICATION NUMBER: US/09/853,033  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: FR 00/12570  
; PRIOR FILING DATE: 2000-10-03  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 660  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric sequence  
; OTHER INFORMATION: Homosapiens-Bacteriophage P1

US-09-853-033-4  
Query Match 98.5%; Score 1231.5; DB 9; Length 660;  
Best Local Similarity 99.2%; Pred. No. 2.5e-117;  
Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 SLALSLTADQVMSALLDAEPPILYSEYDPTPTFSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 370 SLALSLTADQVMSALLDAEPPILYSEYDPTPTFSEASMMGLLTNLADRELVHMINWAKRV 429  
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGVEI 120  
DB 430 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGVEI 489  
QY 121 FDMLLATSSFRMNNLQGEFVCLKSIILLNSGYVTFSLSTLKSLEKDHHRVLDKITD 179  
DB 490 FDMLLATSSFRMNNLQGEFVCLKSIILLNSGYVTFSLSTLKSLEKDHHRVLDKITD 549  
QY 180 TLHLMAKAGLTQQQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 239  
DB 550 TLHLMAKAGLTQQQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 609  
QY 240 DAHRL 244  
DB 610 DAHRL 614

RESULT 13  
US-10-157-899A-8  
; Sequence 8, Application US/10157899A  
; Publication No. US20030143559A1  
; GENERAL INFORMATION:  
; APPLICANT: Bracken, Kathryn Rene  
; APPLICANT: de los Angeles, Joseph Ernest  
; APPLICANT: Huang, Ying  
; APPLICANT: Kadan, Michael Joseph  
; APPLICANT: Keander, Gary Michael  
; APPLICANT: Zerby, Dennis  
; TITLE OF INVENTION: NOVEL ESTROGEN RECEPTOR LIGAND BINDING DOMAIN VARIANTS AND NOVEL  
; FILE REFERENCE: 4-32018A  
; CURRENT APPLICATION NUMBER: US/10/157,899A  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 60/294,839  
; PRIOR FILING DATE: 2001-05-31  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 414  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fusion of a mutated human-Estrogen-receptor-ligand-binding-domain  
; OTHER INFORMATION: and a zinc finger array (C7)

US-10-157-899A-8  
Query Match 98.4%; Score 1230.5; DB 14; Length 414;  
Best Local Similarity 98.8%; Pred. No. 1.7e-117;  
Matches 242; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 SLALSLTADQVMSALLDAEPPILYSEYDPTPTFSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 122 SLALSLTADQVMSALLDAEPPILYSEYDPTPTFSEASMMGLLTNLADRELVHMINWAKRV 181  
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGVEI 120  
DB 182 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGVEI 241  
QY 121 FDMLLATSSFRMNNLQGEFVCLKSIILLNSGYVTFSLSTLKSLEKDHHRVLDKITD 179  
DB 242 FDMLLATSSFRMNNLQGEFVCLKSIILLNSGYVTFSLSTLKSLEKDHHRVLDKITD 301  
QY 180 TLHLMAKAGLTQQQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 239  
DB 302 TLHLMAKAGLTQQQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 361  
QY 240 DAHRL 244  
DB 362 DAHRL 366

RESULT 14  
US-10-157-899A-14  
; Sequence 14, Application US/10157899A  
; Publication No. US20030143559A1  
; GENERAL INFORMATION:  
; APPLICANT: Bracken, Kathryn Rene  
; APPLICANT: de los Angeles, Joseph Ernest  
; APPLICANT: Huang, Ying  
; APPLICANT: Kadan, Michael Joseph  
; APPLICANT: Keander, Gary Michael  
; APPLICANT: Zerby, Dennis  
; TITLE OF INVENTION: NOVEL ESTROGEN RECEPTOR LIGAND BINDING DOMAIN VARIANTS AND NOVEL  
; FILE REFERENCE: 4-32018A  
; CURRENT APPLICATION NUMBER: US/10/157,899A  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 60/294,839

; PRIOR FILING DATE: 2001-05-31  
 ; NUMBER OF SEQ ID NOS: 55  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 14  
 ; LENGTH: 438  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Fusion of a mutated human-Estrogen-receptor-ligand-binding-domain  
 ; OTHER INFORMATION: and a zinc finger array(C7)  
 US-10-157-899A-14

Query Match 98.4%; Score 1230.5; DB 14; Length 438;  
 Best Local Similarity 98.8%; Pred. No. 1.8e-117; Mismatches 1; Indels 1; Gaps 1;  
 Matches 242; Conservative 1; Indels 1; Gaps 1;  
 QY 1 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
 Db 146 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 205  
 QY 61 PGFVDLTLDQVHLLFCAWLEILMIGLVWRSMEHPGKLLFAPNLLIDRNQKCVGMEI 120  
 Db 206 PGFVDLTLDQVHLLFCAWLEILMIGLVWRSMEHPGKLLFAPNLLIDRNQKCVGMEI 265  
 QY 121 FDMLLATSSRRFRMNNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLSEKDHHRVLDKITD 179  
 Db 266 FDMALATSSRRFRMNNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLSEKDHHRVLDKITD 325  
 QY 180 TLIIHLMKAGLTLOQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEML 239  
 Db 326 TLIIHLMKAGLTLOQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEML 385  
 QY 240 DAHRL 244  
 Db 386 DAHRL 390

RESULT 15  
 US-10-006-760-19  
 ; Sequence 19, Application US/10006760  
 ; Publication No. US20030186385A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Koide, Shohel  
 ; TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND  
 ; TITLE OF INVENTION: TO TARGET PROTEINS AND USE THEREOF  
 ; FILE REFERENCE: 176/60901  
 ; CURRENT APPLICATION NUMBER: US/10/006,760  
 ; CURRENT FILING DATE: 2001-11-19  
 ; PCT APPLICATION NUMBER: 60/249,756  
 ; PCT FILING DATE: 2000-11-17  
 ; NUMBER OF SEQ ID NOS: 73  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 19  
 ; LENGTH: 511  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:  
 ; OTHER INFORMATION: lexA-ER(alpha)EF fusion protein  
 US-10-006-760-19

Query Match 98.4%; Score 1230.5; DB 14; Length 511;  
 Best Local Similarity 99.2%; Pred. No. 2.2e-117; Mismatches 0; Indels 1; Gaps 1;  
 Matches 243; Conservative 0; Indels 1; Gaps 1;  
 QY 1 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
 Db 221 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 280  
 QY 61 PGFVDLTLDQVHLLFCAWLEILMIGLVWRSMEHPGKLLFAPNLLIDRNQKCVGMEI 120  
 Db 281 PGFVDLTLDQVHLLFCAWLEILMIGLVWRSMEHPGKLLFAPNLLIDRNQKCVGMEI 340

QY 121 FDMLLATSSRRFRMNNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLSEKDHHRVLDKITD 179  
 Db 341 FDMLLATSSRRFRMNNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLSEKDHHRVLDKITD 400  
 QY 180 TLIIHLMKAGLTLOQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEML 239  
 Db 401 TLIIHLMKAGLTLOQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEML 460  
 QY 240 DAHRL 244  
 Db 461 DAHRL 465

Search completed: November 8, 2004, 08:42:49  
 Job time : 37.849 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2004, 08:16:47 ; Search time 14.4408 Seconds  
(without alignments)  
1120.546 Million cell updates/sec

Title: US-09-830-693B-27

Perfect score: 1250

Sequence: 1 SLALSTADQMSALLDAEP.....CKNVVPLYLLLEMLDAHRL 244

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Sequences: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1239.5	99.2	595	3	US-08-764-870-12
2	1239.5	99.2	595	3	US-08-980-115-12
3	1230.5	98.4	591	2	US-08-836-620A-17
4	1230.5	98.4	595	3	US-09-041-886-35
5	1230.5	98.4	595	4	US-08-453-998-2
6	1230.5	98.4	651	3	US-08-693-940-3
7	1230.5	98.4	651	4	US-09-566-660-3
8	1230.5	98.4	773	3	US-08-564-264-1
9	1213	97.0	410	6	5223606-5
10	1200.5	96.0	596	2	US-08-836-620A-16
11	1179	94.3	264	4	US-09-660-979-1
12	994.5	79.6	243	2	US-08-836-620A-10
13	984.5	78.8	243	2	US-08-836-620A-9
14	979.5	78.4	243	2	US-08-836-620A-8
15	804.5	64.4	575	4	US-09-893-666A-2
16	765.5	61.2	484	2	US-08-836-620A-13
17	765.5	61.2	485	2	US-08-836-620A-2
18	759.5	60.8	477	4	US-09-608-088-5
19	759.5	60.8	477	4	US-09-711-288-5
20	759.5	60.8	485	2	US-08-836-620A-3
21	759.5	60.8	530	4	US-09-608-088-25
22	759.5	60.8	530	4	US-09-711-288-25
23	759.5	60.8	548	3	US-09-139-617-1
24	759.5	60.8	548	4	US-09-561-741A-1
25	759.5	60.8	548	4	US-09-558-795-1
26	751.5	60.1	484	2	US-08-836-620A-14
27	751.5	60.1	485	2	US-08-836-620A-5

Sequence 4, Appli  
Sequence 4, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 7, Appli  
Sequence 15, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 21, Appli  
Sequence 21, Appli  
Sequence 5, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 4, Appli  
Sequence 19, Appli  
Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-08-764-870-12  
; Sequence 12, Application US/08764870  
; Patent No. 6236946  
; GENERAL INFORMATION:  
; APPLICANT: Scanlan, Thomas S  
; APPLICANT: Baxter, John D  
; APPLICANT: Fletcher, Robert J  
; APPLICANT: Wagner, Richard L  
; APPLICANT: Kushner, Peter J  
; APPLICANT: Aprelletti, James W  
; APPLICANT: West, Brian  
; TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward  
; STREET: Five Palo Alto Square, 3000 El Camino Real  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/764,870  
; FILING DATE: 13-DEC-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/008,540  
; FILING DATE: 13-DEC-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/008,543  
; FILING DATE: 13-DEC-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/008,606  
; FILING DATE: 14-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nakamura, Jackie N  
; REGISTRATION NUMBER: 35,966  
; REFERENCE/DOCKET NUMBER: UCAL-246/01US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 843-5000  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 595 amino acids  
; TYPE: amino acid

```
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-764-870-12

Query Match          99.2%; Score 1239.5; DB 3; Length 595;
Best Local Similarity 99.6%; Pred. No. 4.7e-125;
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SLALSITADQVMVSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSITADQVMVSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
QY 61 PGFVDLTLDQVHLLLECAWLEILMTGLVWRSMEHPGKLLFAPNLLDRNQGKVEGMVEI 120
Db 365 PGFVDLTLDQVHLLLECAWLEILMTGLVWRSMEHPGKLLFAPNLLDRNQGKVEGMVEI 424
QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLEEKDHIHRVLDKITYD 179
Db 425 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLEEKDHIHRVLDKITYD 484
QY 180 TLHLMAKAGLTQQQHQRQAQLLLILSHIRMSNKGMEHLYSMKCKNVVPLYDILLEML 239
Db 485 TLHLMAKAGLTQQQHQRQAQLLLILSHIRMSNKGMEHLYSMKCKNVVPLYDILLEML 544
QY 240 DAHRL 244
Db 545 DAHRL 549

RESULT 2
US-08-980-115-12
; Sequence 12, Application US/08980115
; Patent No. 6266622
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Thomas S.
; APPLICANT: Baxter, John D.
; APPLICANT: Fletterick, Robert J.
; APPLICANT: Kushner, Richard L.
; APPLICANT: Wagner, Peter J.
; APPLICANT: Apriletti, James W.
; APPLICANT: West, Brian L.
; APPLICANT: Shiau, Andrew K.
; TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
; FILE REFERENCE: UCAL-246/02US
; CURRENT APPLICATION NUMBER: US/08/980,115
; CURRENT FILING DATE: 1997-11-26
; EARLIER FILING DATE: 1996-12-13
; EARLIER FILING DATE: 1995-12-14
; EARLIER FILING DATE: 1995-12-13
; EARLIER FILING DATE: 1995-12-13
; EARLIER FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (287)..(549)
; OTHER INFORMATION: minimal ligand binding domain
US-08-980-115-12

Query Match          99.2%; Score 1239.5; DB 3; Length 595;
Best Local Similarity 99.6%; Pred. No. 4.7e-125;
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SLALSITADQVMVSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSITADQVMVSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
QY 61 PGFVDLTLDQVHLLLECAWLEILMTGLVWRSMEHPGKLLFAPNLLDRNQGKVEGMVEI 120
Db 365 PGFVDLTLDQVHLLLECAWLEILMTGLVWRSMEHPGKLLFAPNLLDRNQGKVEGMVEI 424
QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLEEKDHIHRVLDKITYD 179
Db 425 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLEEKDHIHRVLDKITYD 484
QY 180 TLHLMAKAGLTQQQHQRQAQLLLILSHIRMSNKGMEHLYSMKCKNVVPLYDILLEML 239
Db 485 TLHLMAKAGLTQQQHQRQAQLLLILSHIRMSNKGMEHLYSMKCKNVVPLYDILLEML 544
QY 240 DAHRL 244
Db 545 DAHRL 549

RESULT 3
US-08-836-620A-17
; Sequence 17, Application US/08836620A
; Patent No. 5958710
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Orphan receptor
; NUMBER OF SEQUENCES: 19
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/08/836,620A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/03933
; FILING DATE:
; APPLICATION NUMBER: GB 9518272.1
; FILING DATE: 08-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9605550.4
; FILING DATE: 15-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9607532.0
; FILING DATE: 11-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9609576.5
; FILING DATE: 08-MAY-1996
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-836-620A-17

Query Match          98.4%; Score 1230.5; DB 2; Length 591;
Best Local Similarity 99.2%; Pred. No. 4.4e-124;
Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 SLALSITADQVMVSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSITADQVMVSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
QY 61 PGFVDLTLDQVHLLLECAWLEILMTGLVWRSMEHPGKLLFAPNLLDRNQGKVEGMVEI 120
Db 365 PGFVDLTLDQVHLLLECAWLEILMTGLVWRSMEHPGKLLFAPNLLDRNQGKVEGMVEI 424
QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLEEKDHIHRVLDKITYD 179
Db 425 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVVTFLLSSTLKSLEEKDHIHRVLDKITYD 484
```

QY 180 TLHLMAKAGLTQQQHQRQAQLLLSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 239  
 DB 485 TLHLMAKAGLTQQQHQRQAQLLLSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 544  
 QY 240 DAHRL 244  
 DB 545 DAHRL 549  
 RESULT 4  
 US-09-041-886-35  
 ; Sequence 35, Application US/09041886  
 ; Patent No. 6235872  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Redesen, Dale E.  
 ; APPLICANT: Rabizadeh, Sharoz  
 ; TITLE OF INVENTION: Proapoptotic Peptides, Dependence  
 ; TITLE OF INVENTION: Polypeptides and Methods of Use  
 ; NUMBER OF SEQUENCES: 72  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Campbell & Flores LLP  
 ; STREET: 4370 La Jolla Village Drive, Suite 700  
 ; CITY: San Diego  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 92122  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/041.886  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Campbell, Cathryn A.  
 ; REGISTRATION NUMBER: 31,815  
 ; REFERENCE/DOCKET NUMBER: P-LJ 2626  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 535-9001  
 ; TELEFAX: (619) 535-8949  
 ; INFORMATION FOR SEQ ID NO: 35:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 595 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: linear  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-041-886-35

Query Match 98.4%; Score 1230.5; DB 3; Length 595;  
 Best Local Similarity 99.2%; Pred. No. 4.4e-124;  
 Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 QY 1 SLALSTADQMSVALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINAKRV 60  
 DB 305 SLALSTADQMSVALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINAKRV 364  
 QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNGKCVGMEI 120  
 DB 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNGKCVGMEI 424  
 QY 121 FDMLLATSSRFPMNLQGFVCLKSIILNLSGVYTFSLSTLSLEKDHHRVLDKITD 179  
 DB 425 FDMLLATSSRFPMNLQGFVCLKSIILNLSGVYTFSLSTLSLEKDHHRVLDKITD 484  
 QY 180 TLHLMAKAGLTQQQHQRQAQLLLSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 239  
 DB 485 TLHLMAKAGLTQQQHQRQAQLLLSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 544  
 QY 240 DAHRL 244  
 DB 545 DAHRL 549

DB 545 DAHRL 549  
 RESULT 5  
 US-08-453-998-2  
 ; Sequence 2, Application US/08453998  
 ; Patent No. 644438  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHAMBON, PIERRE  
 ; APPLICANT: METZGER, DANIEL  
 ; APPLICANT: WHITE, JOHN  
 ; TITLE OF INVENTION: METHOD FOR THE PREPARATION OF A PROTEIN  
 ; TITLE OF INVENTION: BY YEASTS USING AN INDUCIBLE SYSTEM, VECTORS AND  
 ; TITLE OF INVENTION: CORRESPONDING TRANSFORMED STRAINS  
 ; NUMBER OF SEQUENCES: 15  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN, DABBY & CUSHMAN  
 ; STREET: 1100 NEW YORK AVE., N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/453,998  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/161,064  
 ; FILING DATE: 03-DEC-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: CHAPIN, MARLANA K.  
 ; REGISTRATION NUMBER: 35,843  
 ; REFERENCE/DOCKET NUMBER: 1037/98493  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-861-3711  
 ; TELEFAX: 202-822-0944  
 ; TELEX: 6714627 CUSH  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 595 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-453-998-2

Query Match 98.4%; Score 1230.5; DB 4; Length 595;  
 Best Local Similarity 99.2%; Pred. No. 4.4e-124;  
 Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 QY 1 SLALSTADQMSVALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINAKRV 60  
 DB 305 SLALSTADQMSVALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINAKRV 364  
 QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNGKCVGMEI 120  
 DB 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNGKCVGMEI 424  
 QY 121 FDMLLATSSRFPMNLQGFVCLKSIILNLSGVYTFSLSTLSLEKDHHRVLDKITD 179  
 DB 425 FDMLLATSSRFPMNLQGFVCLKSIILNLSGVYTFSLSTLSLEKDHHRVLDKITD 484  
 QY 180 TLHLMAKAGLTQQQHQRQAQLLLSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 239  
 DB 485 TLHLMAKAGLTQQQHQRQAQLLLSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 544  
 QY 240 DAHRL 244  
 DB 545 DAHRL 549

Db 545 DAHRL 549

RESULT 6

US-08-693-940-3

; Sequence 3, Application US/08693940

; Patent No. 6133027

; GENERAL INFORMATION:

; APPLICANT: Yee, Jjing-Kuan

; APPLICANT: Friedman, Theodore

; APPLICANT: Chen, Shin-Tai

; TITLE OF INVENTION: Inducible Expression System

; TITLE OF INVENTION: Useful in the Generation of Packaging Cell Lines for

; TITLE OF INVENTION: Pseudotyped Retroviral Vectors

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bozicevic & Reed, LLP

; STREET: 285 Hamilton Ave, Suite 200

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/693,940

; FILING DATE: 07-AUG-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Francis, Carol L

; REGISTRATION NUMBER: 36,513

; REFERENCE/DOCKET NUMBER: 6510-055001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-327-3400

; TELEFAX: 650-327-3231

; TELEX:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 651 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; AGENT TYPE: internal

US-08-693-940-3

Query Match 98.4%; Score 1230.5; DB 3; Length 651;

Best Local Similarity 99.2%; Pred. No. 5e-124;

Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 SLALSITADQMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60

Db 361 SLALSITADQMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 420

QY 61 PGFVDLTLDQVHLLFCAMLEITMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120

Db 421 PGFVDLTLDQVHLLFCAMLEITMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 480

QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFLLSSTLKSLEEKDHIHRVLDKITD 179

Db 481 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFLLSSTLKSLEEKDHIHRVLDKITD 540

QY 180 TLIIHMAKAGLTLOOQHOLAQLLILSHIRHMSNKGMEHLYSMCKKNVPLYDILLEML 239

Db 541 TLIIHMAKAGLTLOOQHOLAQLLILSHIRHMSNKGMEHLYSMCKKNVPLYDILLEML 600

QY 240 DAHRL 244

Db 601 DAHRL 605

RESULT 8

US-08-564-264-1

; Sequence 1, Application US/08564264

; Patent No. 6040430

; GENERAL INFORMATION:

; APPLICANT: STEWART, Francis

; TITLE OF INVENTION: REGULATION OF SITE-SPECIFIC

; TITLE OF INVENTION: RECOMBINATION BY SITE-SPECIFIC

; TITLE OF INVENTION: RECEPTOR FUSION PROTEINS

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Nikaide, Marmelstein, Murray & Oram

; STREET: 655 Fifteenth Street N.W. Suite 330

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005-5701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

Db 601 DAHRL 605

RESULT 7

US-09-566-660-3

; Sequence 3, Application US/09566660

; Patent No. 6432705

; GENERAL INFORMATION:

; APPLICANT: Yee, Jjing-Kuan

; APPLICANT: Friedman, Theodore

; APPLICANT: Chen, Shin-Tai

; TITLE OF INVENTION: Inducible Expression System

; FILE REFERENCE: 6510-055CON

; CURRENT APPLICATION NUMBER: US/09/566,660

; CURRENT FILING DATE: 2000-05-08

; PRIOR APPLICATION NUMBER: 08/693,940

; PRIOR FILING DATE: 1996-08-07

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 651

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Multi-chimeric transactivating factor

US-09-566-660-3

Query Match 98.4%; Score 1230.5; DB 4; Length 651;

Best Local Similarity 99.2%; Pred. No. 5e-124;

Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 SLALSITADQMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60

Db 361 SLALSITADQMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 420

QY 61 PGFVDLTLDQVHLLFCAMLEITMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120

Db 421 PGFVDLTLDQVHLLFCAMLEITMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 480

QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFLLSSTLKSLEEKDHIHRVLDKITD 179

Db 481 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFLLSSTLKSLEEKDHIHRVLDKITD 540

QY 180 TLIIHMAKAGLTLOOQHOLAQLLILSHIRHMSNKGMEHLYSMCKKNVPLYDILLEML 239

Db 541 TLIIHMAKAGLTLOOQHOLAQLLILSHIRHMSNKGMEHLYSMCKKNVPLYDILLEML 600

QY 240 DAHRL 244

Db 601 DAHRL 605

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/564,264  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP94/02088  
FILING DATE: 28-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 93 110 298.2  
ATTORNEY/AGENT INFORMATION:  
NAME: Murray, Robert B.  
REGISTRATION NUMBER: 22,980  
REFERENCE/DOCKET NUMBER: P564-5019  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)638-5000  
TELEFAX: (202)638-4810  
DRMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 773 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1-423)  
OTHER INFORMATION: /note= "FLP recombinase domain."  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (424-428)  
OTHER INFORMATION: /note= "Linker peptide."  
NAME/KEY: misc feature  
LOCATION: (429-773)  
OTHER INFORMATION: /note= "Estrogen binding domain."  
US-08-564-264-1

Query Match 98.4%; Score 1230.5; DB 3; Length 773;  
Best Local Similarity 99.2%; Pred. No. 6.4e-124;  
Matches 243; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
Qy 1 SLALSLTADQVMSALLDAEPPILYSEYDPTPPFSEASMMGLLTNLADELVHMINWAKRV 60  
Db 483 SLALSLTADQVMSALLDAEPPILYSEYDPTPPFSEASMMGLLTNLADELVHMINWAKRV 542  
Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQGKCVGMEI 120  
Db 543 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQGKCVGMEI 602  
Qy 121 FDMLLATSSRRFMNLOQ-EFVCLKSIILLNSGYVTFSLSTLKSLEEKDHIHRVLDKITD 179  
Db 603 FDMLLATSSRRFMNLOQ-EFVCLKSIILLNSGYVTFSLSTLKSLEEKDHIHRVLDKITD 662  
Qy 180 TLIHMAKAGITLQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 239  
Db 663 TLIHMAKAGITLQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 722  
Qy 240 DAHRL 244  
Db 723 DAHRL 727

RESULT 9  
5223606-5  
Patent No. 5223606  
APPLICANT: BLAUDIN DE THE, HUGHES;MARCHIO, AGNES;TIOILLAIS,  
PIERRE;DEJEAN, ANNE  
TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED  
PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA  
NUMBER OF SEQUENCES: 11  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/134,130  
FILING DATE: 17-DEC-1987  
PRIOR APPLICATION DATA:  
SEQ ID NO.5:  
LENGTH: 410  
5223606-5  
Query Match 97.0%; Score 1213; DB 6; Length 410;  
Best Local Similarity 98.8%; Pred. No. 2e-122;  
Matches 242; Conservative 0; Mismatches 1; Indels 2; Gaps 2;  
Qy 1 SLALSLTADQVMSALLDAEPPILYSEYDPTPPFSEASMMGLLTNLADELVHMINWAKRV 60  
Db 121 SLALSLTADQVMSALLDAE-PILYSEYDPTPPFSEASMMGLLTNLADELVHMINWAKRV 179  
Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQGKCVGMEI 120  
Db 180 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQGKCVGMEI 239  
Qy 121 FDMLLATSSRRFMNLOQ-EFVCLKSIILLNSGYVTFSLSTLKSLEEKDHIHRVLDKITD 179  
Db 240 FDMLLATSSRRFMNLOQ-EFVCLKSIILLNSGYVTFSLSTLKSLEEKDHIHRVLDKITD 299  
Qy 180 TLIHMAKAGITLQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 239  
Db 300 TLIHMAKAGITLQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEML 359  
Qy 240 DAHRL 244  
Db 360 DAHRL 364  
RESULT 10  
US-08-836-620A-16  
Sequence 16, Application US/08836620A  
Patent No. 5958710  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Orphan receptor  
NUMBER OF SEQUENCES: 19  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA: US/08/836,620A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP96/03933  
FILING DATE:  
APPLICATION NUMBER: GB 9518272.1  
FILING DATE: 08-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9605550.4  
FILING DATE: 15-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9607532.0  
FILING DATE: 11-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9609576.5  
FILING DATE: 08-MAY-1996  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 596 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Rattus rattus  
US-08-836-620A-16  
Query Match 96.0%; Score 1200.5; DB 2; Length 596;  
Best Local Similarity 95.9%; Pred. No. 7.7e-121;

Matches	235;	Conservative	5;	Mismatches	4;	Indels	1;	Gaps	1;
Qy	1	SLALSLTADQMVSALLDAEPPILYSEYPDTPRPFSEASMMGLTTLNLADELVHMINWAKRV	60	:                     :                     :					
Dd	310	SPALSLTADQMVSALLDAEPPILYSEYPDPSRPFSSEASMMGLTTLNLADELVHMINWAKRV	369	:                     :                     :					
Qy	61	PGFVDLTLHDQVHLLECAWLIELMIGLVWRSMHPGKLLFAPNLILLDRNQCKVEGMVEI	120	:                     :                     :					
Dd	370	PGFGDLNLHDQVHLLECAWLIELMIGLVWRSMHPGKLLFAPNLILLDRNQCKVEGMVEI	429	:                     :                     :					
Qy	121	FDMLLATSSRFPMNNLOQ-BEVCLUKSIILLNSGVVTFLSSTLKSEKDHIHRVLDKITD	179	:                     :                     :					
Dd	430	FDMLLATSSRFPMNNLOQEFPVCUKSIILLNSGVVTFLSSTLKSEKDHIHRVLDKIND	489	:                     :                     :					
Qy	180	TLIHLMAGAGLTQQOQHRLAQLLLLISHIRHMSNMKGMEHYLSMKCNVVPLYDLLLEML	239	:                     :                     :					
Dd	490	TLIHLMAGAGLTQQOQHRLAQLLLLISHIRHMSNMKGMEHYLYNMCKNVVPLYDLLLEML	549	:                     :                     :					
Qy	240	DAHRL 244 							
Dd	550	DAHRL 554 							
RESULT 11									
US-09-660-979-1									
; Sequence 1, Application US/09660979									
; Patent No. 6500629									
; GENERAL INFORMATION:									
; APPLICANT: Cleaver, Brian									
; APPLICANT: Green, Mike L.									
; TITLE OF INVENTION: Materials and Methods for Detection and Quantitation of									
; FILE REFERENCE: ELI-101XCI									
; CURRENT APPLICATION NUMBER: US/09/660,979									
; PRIORITY FILING DATE: 2000-09-13									
; PRIOR APPLICATION NUMBER: 60/153,627									
; PRIOR FILING DATE: 1999-09-13									
; NUMBER OF SEQ ID NOS: 1									
; SOFTWARE: Patentin version 3.0									
; SEQ ID NO 1									
; LENGTH: 264									
; TYPE: Prt									
; ORGANISM: Equus									
US-09-660-979-1									

```

;
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Orphan receptor
; NUMBER OF SEQUENCES: 19
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,620A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/03933
; FILING DATE:
; APPLICATION NUMBER: GB 9518272.1
; FILING DATE: 08-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9605550.4
; FILING DATE: 15-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9607532.0
; FILING DATE: 11-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9609576.5
; FILING DATE: 08-MAY-1996
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; ORGANISM: Homo sapiens
; US-08-836-620A-10

Query Match 79.6%; Score 994.5; DB 2; Length
Best Local Similarity 99.0%; Pred. No. 3.7e-99;
Matches 195; Conservative 0; Mismatches 1; Indel

Qy 49 ELVHMNNAKRVGFGVDLTLDHQVHLLCAWLEILMIGLVWRSMEH
Db 1 ELVHMNNAKRVGFGVDLTLDHQVHLLCAWLEILMIGLVWRSMEH
Qy 109 NQCKVCEGVNVEIFDMLLATSSRFMMNLQG-EFVCLKSIILILNSGV
Db 61 NQCKVCEGVNVEIFDMLLATSSRFMMNLQGEFVCLKSIILILNSGV
Qy 168 DHIHRVLDKITDTLTIHLMAKAGLTIQQQHQRLAQLLLTSLHIRMMSH
Db 121 DHIHRVLDKITDTLTIHLMAKAGLTIQQQHQRLAQLLLTSLHIRMMSH
Qy 228 VVPLYDLLLEMLDAHRL 244
Db 181 VVPLYDLLLEMLDAHRL 197

RESULT 13
US-08-836-620A-9
; Sequence 9, Application US/08836620A
; Patent No. 5958710
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Orphan receptor
; NUMBER OF SEQUENCES: 19
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,620A
; FILING DATE:
; PRIOR APPLICATION DATA:

```



```

; APPLICATION NUMBER: PCT/EP96/03933
; FILING DATE:
; APPLICATION NUMBER: GB 9518272.1
; FILING DATE: 08-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9605550.4
; FILING DATE: 15-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9607532.0
; FILING DATE: 11-APR-1996
; APPLICATION NUMBER: GB 9609576.5
; FILING DATE: 08-MAY-1996
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; ORGANISM: Mus musculus
; US-836-620A-9

Query Match      78.8%; Score 984.5; DB 2; Length 243;
Best Local Similarity 97.5%; Pred. No. 4.4e-98;
Matches 192; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 49 ELVHMINWAKRVPGFVDLTLLHDOVHLLLECAWLEITMIGLVWRSMEHPGKLLFAPNLLDR 108
DB 1 ELVHMINWAKRVPGFVDLTLLHDOVHLLLECAWLEITMIGLVWRSMEHPGKLLFAPNLLDR 60

QY 109 NOGKCEGVMEIFDMLLATSRRFRMNLQ- EFVCLKSIILLNSGVYTFLSSTLKSLEEK 167
DB 61 NOGKCEGVMEIFDMLLATSRRFRMNLQEEFVCLKSIILLNSGVYTFLSSTLKSLEEK 120

QY 168 DHHRVLDKITDTHLHMAKAGTLQOOHORLAQLLILSHIRHMSKMGHEHLYSMCKN 227
DB 121 DHHRVLDKITDTHLHMAKAGTLQOOHORLAQLLILSHIRHMSKMGHEHLYSMCKN 180

QY 228 VVPLYDLLLLEMLDAHRL 244
DB 181 VVPLYDLLLLEMLDAHRL 197

RESULT 14
US-836-620A-8
; Sequence 8, Application US/08836620A
; Patent No. 5958710
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Orphan receptor
; NUMBER OF SEQUENCES: 19
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,620A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/03933
; FILING DATE:
; APPLICATION NUMBER: GB 9518272.1
; FILING DATE: 08-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9605550.4
; FILING DATE: 15-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9607532.0
; FILING DATE: 11-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9609576.5
; FILING DATE: 08-MAY-1996

```

```

; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Rattus rattus
; US-08-836-620A-8

Query Match      78.4%; Score 979.5; DB 2; Length 243;
Best Local Similarity 97.0%; Pred. No. 1.5e-97;
Matches 191; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 49 ELVHMINWAKRVPGFVDLTLLHDOVHLLLECAWLEITMIGLVWRSMEHPGKLLFAPNLLDR 108
DB 1 ELVHMINWAKRVPGFVDLTLLHDOVHLLLECAWLEITMIGLVWRSMEHPGKLLFAPNLLDR 60

QY 109 NOGKCEGVMEIFDMLLATSRRFRMNLQ- EFVCLKSIILLNSGVYTFLSSTLKSLEEK 167
DB 61 NOGKCEGVMEIFDMLLATSRRFRMNLQEEFVCLKSIILLNSGVYTFLSSTLKSLEEK 120

QY 168 DHHRVLDKITDTHLHMAKAGTLQOOHORLAQLLILSHIRHMSKMGHEHLYSMCKN 227
DB 121 DHHRVLDKITDTHLHMAKAGTLQOOHORLAQLLILSHIRHMSKMGHEHLYSMCKN 180

QY 228 VVPLYDLLLLEMLDAHRL 244
DB 181 VVPLYDLLLLEMLDAHRL 197

RESULT 15
US-09-893-666A-2
; Sequence 2, Application US/09893666A
; Patent No. 6759568
; GENERAL INFORMATION:
; APPLICANT: YAWASHITA, ICHIRO
; TITLE OF INVENTION: High estrogen-sensitive medaka fish
; FILE REFERENCE: 210217US-620-7249-0
; CURRENT APPLICATION NUMBER: US/09/893,666A
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: JP 2000-247729
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 575
; ORGANISM: Oryzias latipes
; US-09-893-666A-2

Query Match      64.4%; Score 804.5; DB 4; Length 575;
Best Local Similarity 63.9%; Pred. No. 4e-78;
Matches 154; Conservative 42; Mismatches 44; Indels 1; Gaps 1;

QY 5 SUTADQWSALLDAEPPILSYDPTPTFSEASMMGLTNLADRELVHMINWAKRVPGFV 64
DB 268 SIPPEQVILLLOQAEPPILCSRQKLSRPYTEVTMTLLTSMADKELVHMINWAKRVPGFL 327

QY 65 DLTLDHDOVHLLLECAWLEITMIGLVWRSMEHPGKLLFAPNLLDRNQGKCEGVMEIFDML 124
DB 328 QLSLDHDOVHLLLESSWLEVMIGLWRSIHCPGKLIQAQLILDNRNQGDCVEGMEIFDML 387

QY 125 LATSSRRFRMNLQ-GEFVCLKSIILLNSGVYTFLSSTLKSLEKDHHRVLDKITDTHLH 183
DB 388 LATASRFVLKLPKEEFVCLKSIILLNSGAFSECTGTMBPLHNSAAVQSMDDITDALIH 447

QY 184 LMAKAGTLQOOHORLAQLLILSHIRHMSKMGHEHLYSMCKNVPLVDLLEMLDAHR 243
DB 448 YISQSGYLAQEQARQAQLLILSHIRHMSKMGHEHLYSMCKNVPLVDLLEMLDAHR 507

QY 244 L 244
DB 508 L 508

```

Search completed: November 8, 2004, 08:29:27  
Job time : 15.4408 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2004, 08:04:31 ; Search time 58.7592 Seconds  
(without alignments)  
1489.639 Million cell updates/sec

Title: US-09-830-693B-27

Perfect score: 1250

Sequence: 1 SLALSLTADQMSALLDAEP.....CKNVVPLYDLLEMLDAHRL 244

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Sequences: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1239.5	99.2	414	6 AAE35275	Aae35275 C7LBDAS f
2	1239.5	99.2	422	4 AAB61498	Aab61498 Protein e
3	1239.5	99.2	438	6 AAE35276	Aae35276 C7LBDAS f
4	1239.5	99.2	457	4 AAB61499	Aab61499 Protein e
5	1239.5	99.2	480	4 AAB36684	Aab36684 Mammalian
6	1239.5	99.2	595	2 AAY21626	Aay21626 Ligand bi
7	1239.5	99.2	595	4 AAG84505	Ag84505 Human oes
8	1239.5	99.2	595	4 AAG84513	Ag84513 Human oes
9	1239.5	99.2	595	4 AAG84506	Ag84506 Human oes
10	1239.5	99.2	595	5 ABB76378	Abb76378 Human nuc
11	1239.5	99.2	595	8 ADP05661	Adp05661 Human nuc
12	1239.5	99.2	595	8 ADO42788	Ado42788 Wild type
13	1239.5	99.2	595	8 ADO42830	Ado42830 Human oes
14	1235.5	98.8	244	3 AAB26784	Aab26784 Oestrogen
15	1235.5	98.8	244	3 AAB26780	Aab26780 Human oes
16	1235.5	98.8	595	4 AAG84509	Ag84509 Human oes
17	1235.5	98.8	595	8 ADO42815	Ado42815 Mutant hu
18	1234.5	98.8	595	8 ADO42820	Ado42820 Mutant hu
19	1233.5	98.7	246	5 ABJ15106	Abj15106 LBDG1 rel
20	1233.5	98.7	595	4 AAG84507	Ag84507 Human oes
21	1233.5	98.7	595	8 ADO42789	Ado42789 Mutant hu
22	1232.5	98.6	595	4 AAG84508	Ag84508 Human oes
23	1232.5	98.6	595	4 AAG84514	Ag84514 Human oes
24	1231.5	98.5	595	4 AAG84512	Ag84512 Human oes
25	1231.5	98.5	660	5 ABB76379	Abb76379 Cre recom

26	1230.5	98.4	347	5 ABP70164	Abp70164 Amino aci
27	1230.5	98.4	414	6 AAE35278	Aae35278 C7LBDAS f
28	1230.5	98.4	438	6 AAE35281	Aae35281 C7LBDAS f
29	1230.5	98.4	511	7 ADE39222	Ad39222 LexA-oes
30	1230.5	98.4	547	5 AAU98984	Aau98984 Oestrogen
31	1230.5	98.4	589	7 ADB99352	Adb99352 Fusion pr
32	1230.5	98.4	595	2 AAY33506	Aay33506 Human oes
33	1230.5	98.4	595	4 AAG84511	Ag84511 Human oes
34	1230.5	98.4	595	4 AAG84510	Ag84510 Human oes
35	1230.5	98.4	595	5 AAG68251	Ag68251 Human oes
36	1230.5	98.4	595	5 AAU98987	Aau98987 Oestrogen
37	1230.5	98.4	595	5 AAU98983	Aau98983 Oestrogen
38	1230.5	98.4	595	5 AAU98988	Aau98988 Oestrogen
39	1230.5	98.4	595	5 ABB09265	Abb09265 Human oes
40	1230.5	98.4	595	5 ABP70163	Abp70163 Amino aci
41	1230.5	98.4	595	5 ABB81783	Abb81783 Human oes
42	1230.5	98.4	595	6 ABG76090	Abg76090 Human oes
43	1230.5	98.4	595	6 ABR47448	Ab47448 Breast ca
44	1230.5	98.4	595	6 ABU09033	Abu09033 Human oes
45	1230.5	98.4	595	6 AAE35283	Aae35283 Human wil

ALIGNMENTS

RESULT 1

AAE35275

ID AAE35275 standard; protein; 414 AA.

AC AAE35275;

XX

XX

DT 28-MAY-2003 (first entry)

XX

DE C7LBDAS fusion (wild-type) protein.

XX

KW Oestrogen receptor; ER alpha; ligand binding domain; genetic disease;  
acquired disease; cell proliferative disorder; cancer; adenocarcinoma;  
LBD; gene switch; transgenic animal; transgenic; gene therapy; human;  
zinc finger array; C7; fusion protein.

XX

OS Homo sapiens.

OS Unidentified.

OS Chimeric.

XX

PN WO200297050-A2.

XX

PD 05-DEC-2002.

XX

PF 31-MAY-2002; 2002WO-US016946.

XX

PR 31-MAY-2001; 2001US-0294839P.

XX

PA (NOVS ) NOVARTIS AG.

XX

PI Bracken KR, De Los Angeles JE, Huang Y, Kadan MJ, Ksander GM;

PI Zerby DB;

XX

DR WPI; 2003-156794/15.

DR

DR N-PSDB; AAU53875.

XX

PT New mutant estrogen receptor ligand binding domain capable of interacting

PT with non-endogenous ligand, useful e.g. in combination with a ligand for

PT constructing selective molecular gene switches for regulating gene

PT function.

XX

PS Example 4; Page 117-118; 159pp; English.

XX

CC The invention relates to a mutant oestrogen receptor (ER) alpha-ligand

CC binding domain (LBD) which comprises an amino acid modification in region

CC 1, region 2 or both and interacting with a non-endogenous ligand as a

CC result of the amino acid modification. Sequences of the invention are a

CC useful for treatment of genetic diseases, acquired diseases and any other

CC conditions including cell proliferative disorders such as cancer e.g.

CC lung, breast, lymphoid, gastrointestinal, genito-urinary tract  
CC adenocarcinomas and other malignancies such as colon cancers, renal- cell  
CC carcinoma, prostate cancer, non-small cell carcinoma of the lung, cancer  
CC of the small intestine and cancer of the oesophagus. The invention is  
CC useful for constructing selective molecular gene switches for regulating  
CC gene function in plants and transgenic animals. It is also useful in gene  
CC therapy. The present sequence is human ER alpha LBD -zinc finger array  
CC (C7) fusion protein  
XX  
SQ Sequence 414 AA;

Query Match 99.2%; Score 1239.5; DB 6; Length 414;  
Best Local Similarity 99.6%; Pred. No. 2.1e-124;  
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 SLALSITADQVMSALLDAEPPILYSEYDTPFPFSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 122 SLALSITADQVMSALLDAEPPILYSEYDTPFPFSEASMMGLLTNLADRELVHMINWAKRV 181  
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 120  
DB 182 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 241  
QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVVTFLSSTLKSLEEKDHIHRVLDKITD 179  
DB 242 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVVTFLSSTLKSLEEKDHIHRVLDKITD 301  
QY 180 TLHLMAKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEML 239  
DB 302 TLHLMAKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEML 361  
QY 240 DAHRL 244  
DB 362 DAHRL 366

RESULT 2  
AAB61498  
ID AAB61498 standard; protein; 422 AA.  
AC AAB61498;  
DT 04-APR-2001 (first entry)  
DE Protein encoded by human estrogen receptor alpha isoform #1.  
XX Human; estrogen receptor alpha; cancer; osteoporosis; bone; Alzheimer's;  
KW Human; estrogen receptor alpha; cancer; osteoporosis; bone; Alzheimer's;  
KW cardiovascular.  
XX Homo sapiens.  
OS  
PN WO200100823-A1.  
XX  
XX 04-JAN-2001.  
XX  
XX 27-JUN-2000; 2000WO-EP005981.  
XX  
XX 29-JUN-1999; 99IT-MI001433.  
PR (EUMO-) EURO MOLECULAR BIOLOGY LAB.  
PA  
XX Gannon F, Denger S, Flouriot G;  
PI  
XX WPI; 2001-137955/14.  
DR  
XX Novel isoforms of human estrogen receptor alpha useful for preparing  
PT therapeutic agents for treating cancer, osteoporosis, Alzheimer's disease  
PT and cardiovascular diseases.  
XX  
XX Claim 4; Page 45-46; 53pp; English.  
PS  
XX The present invention relates to a human estrogen receptor (HER)-alpha  
CC isoform. Molecules which modulate the activity of the estrogen receptor  
CC

CC are useful for the preparation of therapeutic agents for treating cancer,  
CC osteoporosis and other bone disorders, Alzheimer's disease and  
XX cardiovascular diseases  
SQ Sequence 422 AA;

Query Match 99.2%; Score 1239.5; DB 4; Length 422;  
Best Local Similarity 99.6%; Pred. No. 2.2e-124;  
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 SLALSITADQVMSALLDAEPPILYSEYDTPFPFSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 132 SLALSITADQVMSALLDAEPPILYSEYDTPFPFSEASMMGLLTNLADRELVHMINWAKRV 191  
QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 120  
DB 192 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 251  
QY 121 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVVTFLSSTLKSLEEKDHIHRVLDKITD 179  
DB 252 FDMLLATSSRRFRMMNLQGEFVCLKSIILLNSGVVTFLSSTLKSLEEKDHIHRVLDKITD 311  
QY 180 TLHLMAKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEML 239  
DB 312 TLHLMAKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEML 371  
QY 240 DAHRL 244  
DB 372 DAHRL 376

RESULT 3  
AAE35276  
ID AAE35276 standard; protein; 438 AA.  
XX  
AC AAE35276;  
DT 28-MAY-2003 (first entry)  
XX  
DE C7LBDBS fusion (wild-type) protein.  
XX  
KW Oestrogen receptor; ER alpha; ligand binding domain; genetic disease;  
KW acquired disease; cell proliferative disorder; cancer; adenocarcinoma;  
KW LBD; gene switch; transgenic animal; transgenic; gene therapy; human;  
KW zinc finger array; C7; fusion protein.  
XX  
XX Homo sapiens.  
OS Unidentified.  
OS Chimeric.  
XX  
PN WO200297050-A2.  
XX  
PD 05-DEC-2002.  
XX  
XX 31-MAY-2002; 2002WO-US016946.  
PF  
XX 31-MAY-2001; 2001US-0294839P.  
XX  
XX (NOVS ) NOVARTIS AG.  
XX  
XX Bracken KR, De Los Angeles JE, Huang Y, Kadan MJ, Ksander GM;  
PI Zerby DB;  
XX  
XX WPI; 2003-156794/15.  
DR N-PSDB; AAD53876.  
XX  
XX New mutant estrogen receptor ligand binding domain capable of interacting  
PT with non-endogenous ligand, useful e.g. in combination with a ligand for  
PT constructing selective molecular gene switches for regulating gene  
PT function.  
XX  
XX Example 4; Page 120-122; 159pp; English.  
PS  
XX

CC The invention relates to a mutant oestrogen receptor (ER) alpha-ligand  
CC binding domain (LBD) which comprises an amino acid modification in region  
CC 1, region 2 or both and interacting with a non-endogenous ligand as a  
CC result of the amino acid modification. Sequences of the invention are  
CC useful for treatment of genetic diseases, acquired diseases and any other  
CC conditions including cell proliferative disorders such as cancer e.g.  
CC lung, breast, lymphoid, gastrointestinal, genito-urinary tract  
CC adenocarcinomas and other malignancies such as colon cancers, renal- cell  
CC carcinoma, prostate cancer, non-small cell carcinoma of the lung, cancer  
CC of the small intestine and cancer of the oesophagus. The invention is  
CC useful for constructing selective molecular gene switches for regulating  
CC gene function in plants and transgenic animals. It is also useful in gene  
CC therapy. The present sequence is human ER alpha LBD -zinc finger array  
CC (C7) fusion protein  
XX  
SQ Sequence 438 AA;

Query Match 99.2%; Score 1239.5; DB 6; Length 438;  
Best Local Similarity 99.6%; Pred. No. 2.3e-124;  
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 SLALSLTADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINAKRV 60  
DB 146 SLALSLTADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINAKRV 205  
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVRSMEHPGKLLFAPNLLDRNOGKCVGMEI 120  
DB 206 PGFVDLTLDQVHLLCAWLEILMIGLVRSMEHPGKLLFAPNLLDRNOGKCVGMEI 265  
QY 121 FDMLLATSSRRFMNLOG-EFVCLKSIILLNSGYTFLSSTLSLEEKDHIHRVLDKITD 179  
DB 266 FDMLLATSSRRFMNLOG-EFVCLKSIILLNSGYTFLSSTLSLEEKDHIHRVLDKITD 325  
QY 180 TLHLMAKAGLTLOOQHORAQLLLILSHIRHNSKGMHELYSMKCKNVVPLVDLLEML 239  
DB 326 TLHLMAKAGLTLOOQHORAQLLLILSHIRHNSKGMHELYSMKCKNVVPLVDLLEML 385  
QY 240 DAHRL 244  
DB 386 DAHRL 390

RESULT 4  
AAB61499  
ID AAB61499 standard; protein; 457 AA.  
XX  
AC AAB61499;  
XX  
DE 04-APR-2001 (first entry)  
XX  
DE Protein encoded by human estrogen receptor alpha isoform #2.  
XX  
KW Human; estrogen receptor alpha; cancer; osteoporosis; bone; Alzheimer's;  
KW cardiovascular.  
XX  
OS Homo sapiens.  
XX  
PN WO200100823-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 27-JUN-2000; 2000WO-EP005981.  
XX  
PR 29-JUN-1999; 99IT-MI001433.  
XX  
PA (EUMO-) EURO MOLECULAR BIOLOGY LAB.  
XX  
PI Gannon F, Dengler S, Flouriot G;  
XX  
DR WPI; 2001-137955/14.  
XX  
PT Novel isoforms of human estrogen receptor alpha useful for preparing  
PT therapeutic agents for treating cancer, osteoporosis, Alzheimer's disease

PT and cardiovascular diseases.  
XX  
PS Claim 4; Page 46-48; 53pp; English.  
XX

CC The present invention relates to a human estrogen receptor (hER)-alpha  
CC isoform. Molecules which modulate the activity of the estrogen receptor  
CC are useful for the preparation of therapeutic agents for treating cancer,  
CC osteoporosis and other bone disorders, Alzheimer's disease and  
CC cardiovascular diseases  
XX  
SQ Sequence 457 AA;

Query Match 99.2%; Score 1239.5; DB 4; Length 457;  
Best Local Similarity 99.6%; Pred. No. 2.4e-124;  
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 SLALSLTADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINAKRV 60  
DB 167 SLALSLTADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINAKRV 226  
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVRSMEHPGKLLFAPNLLDRNOGKCVGMEI 120  
DB 227 PGFVDLTLDQVHLLCAWLEILMIGLVRSMEHPGKLLFAPNLLDRNOGKCVGMEI 286  
QY 121 FDMLLATSSRRFMNLOG-EFVCLKSIILLNSGYTFLSSTLSLEEKDHIHRVLDKITD 179  
DB 287 FDMLLATSSRRFMNLOG-EFVCLKSIILLNSGYTFLSSTLSLEEKDHIHRVLDKITD 346  
QY 180 TLHLMAKAGLTLOOQHORAQLLLILSHIRHNSKGMHELYSMKCKNVVPLVDLLEML 239  
DB 347 TLHLMAKAGLTLOOQHORAQLLLILSHIRHNSKGMHELYSMKCKNVVPLVDLLEML 406  
QY 240 DAHRL 244  
DB 407 DAHRL 411

RESULT 5  
AAB36684  
ID AAB36684 standard; protein; 480 AA.  
XX  
AC AAB36684;  
XX  
DE 15-MAR-2001 (first entry)  
XX  
DE Mammalian two-hybrid protein SEQ ID NO:8.  
XX  
KW Mammalian; two-hybrid assay; hybrid protein; hybrid gene; detection;  
KW reporter gene; DNA-binding region; transcriptional activation;  
KW fused protein; protein interaction.  
XX  
OS Mammalia.  
OS Synthetic.  
XX  
PN WO200071743-A1.  
XX  
PD 30-NOV-2000.  
XX  
PF 25-MAY-2000; 2000WO-JP003353.  
XX  
PR 25-MAY-1999; 99JP-00144946.  
XX  
PA (EISA ) EISAI CO LTD.  
XX  
PI Tsukahara K, Hida T, Nakamura K, Yoshitomi H;  
XX  
DR WPI; 2001-025169/03.  
DR N-PSDB; AAC88199.  
XX  
PT Novel two hybrid detection method comprising fusing two proteins with a  
PT DNA binding sequence and a transcription activation sequence respectively  
PT for detecting interaction of the proteins in mammalian cells.  
XX

PS Example 2; Page 35-37; 63pp; Japanese.  
 XX The present invention describes a method for detecting the interaction of  
 CC a first and a second protein within a mammalian cell. The method  
 CC comprises a fusion protein of the first protein with two or more  
 CC transcription activation sequences (which may be the same or different),  
 CC and a fusion protein of the second protein with a DNA-binding sequence.  
 CC These are expressed in a mammalian cell containing a DNA carrying a  
 CC reporter gene downstream of a sequence binding to the DNA-binding  
 CC sequence; and the expression of the reporter gene is detected to indicate  
 CC interaction of the two proteins. The method is useful for the  
 CC identification and examination of protein interactions within the  
 CC mammalian cell, and screening of potential drugs targeting them. The  
 CC present sequence represents a hybrid protein from an example given in the  
 CC present invention  
 XX  
 SQ Sequence 480 AA;

Query Match 99.2%; Score 1239.5; DB 4; Length 480;  
 Best Local Similarity 99.6%; Pred. No. 2.6e-124;  
 Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 SLALSITADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
 DB 174 SLALSITADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 233  
 QY 61 PGFVDLTLDQVHLLLECAWLEITMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120  
 DB 234 PGFVDLTLDQVHLLLECAWLEITMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 293  
 QY 121 FDMLLATSSRRFMNMQG-EFVCLSKIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179  
 DB 294 FDMLLATSSRRFMNMQG-EFVCLSKIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 353  
 QY 180 TLIHLMKAGLTLOQHQHQLAQLLLILSHIRHMSNKGMEHLYSMCKKNVPLYDLLEML 239  
 DB 354 TLIHLMKAGLTLOQHQHQLAQLLLILSHIRHMSNKGMEHLYSMCKKNVPLYDLLEML 413  
 QY 240 DAHRL 244  
 DB 414 DAHRL 418

RESULT 6  
 AAY21626  
 ID AAY21626 standard; protein; 595 AA.  
 XX  
 AC AAY21626;  
 DT -AUG-1999 (first entry)  
 DE Ligand binding domain of nuclear receptor HER.  
 KW Thyroid hormone receptor; aromatic compound; ligand binding domain;  
 KW alpha-glycerophosphate dehydrogenase; cardiac; obesity; triglyceride;  
 KW plasma cholesterol; anti-hypertriglyceridaemic; atherosclerosis; GPDH;  
 KW thyroid hormone replacement therapy; nuclear receptor.  
 XX  
 OS Homo sapiens.  
 XX WO926966-A2.  
 PN 03-JUN-1999.  
 XX 25-NOV-1998; 98WO-US025296.  
 PR 26-NOV-1997; 97US-00980115.  
 XX (REG ) UNIV CALIFORNIA.  
 XX Scanlan TS, Baxter JD, Fletterick RJ, Wagner RL, Kushner PJ;  
 PI Aprilletti JW, West BL, Shiau AK;

DR WPI; 1999-357810/30.  
 XX Modulating activity of a thyroid hormone receptor.  
 PS Disclosure; Fig 3G-R; 447pp; English.  
 CC The invention relates to a method for modulating activity of a thyroid  
 CC hormone receptor that comprises administration of an aromatic compound  
 CC which fits spatially and preferentially into a thyroid hormone ligand  
 CC binding domain. The aromatic compound (of a specified formula) can be  
 CC used to increase alpha-glycerophosphate dehydrogenase (GPDH) levels, at  
 CC levels which do not significantly modify cardiac GPDH levels and are  
 CC indicated in the treatment of obesity. The compound also lower total  
 CC plasma cholesterol and triglyceride levels and can be used as anti-  
 CC hypertriglyceridaemic agents. The compound may also be used for treating  
 CC atherosclerosis and may be indicated in thyroid hormone replacement  
 CC therapy in patients with compromised cardiac function. Sequences AAY21621  
 CC - 636 amino acid sequences of ligand binding domains of several members  
 CC of the nuclear receptor superfamily  
 XX  
 SQ Sequence 595 AA;

Query Match 99.2%; Score 1239.5; DB 2; Length 595;  
 Best Local Similarity 99.6%; Pred. No. 3.5e-124;  
 Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 SLALSITADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
 DB 305 SLALSITADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364  
 QY 61 PGFVDLTLDQVHLLLECAWLEITMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 120  
 DB 365 PGFVDLTLDQVHLLLECAWLEITMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEI 424  
 QY 121 FDMLLATSSRRFMNMQG-EFVCLSKIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179  
 DB 425 FDMLLATSSRRFMNMQG-EFVCLSKIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484  
 QY 180 TLIHLMKAGLTLOQHQHQLAQLLLILSHIRHMSNKGMEHLYSMCKKNVPLYDLLEML 239  
 DB 485 TLIHLMKAGLTLOQHQHQLAQLLLILSHIRHMSNKGMEHLYSMCKKNVPLYDLLEML 544  
 QY 240 DAHRL 244  
 DB 545 DAHRL 549

RESULT 7  
 AAG84505  
 ID AAG84505 standard; protein; 595 AA.  
 XX  
 AC AAG84505;  
 DT 10-SEP-2001 (first entry)  
 DE Human oestrogen receptor alpha protein.  
 KW Ligand dependent transcriptional factor; oestrogen receptor; ER;  
 KW glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;  
 KW MR; peroxisome proliferator-activated receptor protein; PPAR;  
 KW progesterone receptor protein; PR; pregnane X receptor protein; PXR;  
 KW thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;  
 KW transactivation; Eralpha; breast cancer.  
 OS Homo sapiens.  
 XX WO200142307-A1.  
 PN 14-JUN-2001.  
 XX 01-DEC-2000; 2000WO-JP008553.  
 XX 07-DEC-1999; 99JP-00348022.

PR 27-DEC-1999; 99JP-00370667.  
 PR 07-JUL-2000; 2000JP-00207011.  
 PR 21-JUL-2000; 2000JP-00220508.  
 PR 02-AUG-2000; 2000JP-00234053.  
 PR 03-AUG-2000; 2000JP-00235460.  
 PR 03-AUG-2000; 2000JP-00235461.  
 PR 03-AUG-2000; 2000JP-00235463.  
 XX (SUMO ) SUMITOMO CHEM CO LTD.  
 XX Saito K, Ohe N, Satoh H;  
 XX WPI; 2001-367866/38.  
 XX  
 PT Ligand dependent transcriptional factors, nuclear acids encoding them and  
 PT cells comprising them and a specified reporter gene, useful for screening  
 PT agents for the treatment of breast cancer.  
 XX  
 PS Claim 7; Page 167-170; 276pp; English.  
 XX  
 CC The present invention relates to ligand dependent transcriptional factors  
 CC including oestrogen receptor (ER) alpha and beta protein, glucocorticoid  
 CC receptor protein (GR), mineralocorticoid receptor protein (MR),  
 CC peroxisome proliferator-activated receptor protein (PPAR), progesterone  
 CC receptor protein (PR), pregnane X receptor protein (PXR), thyroid hormone  
 CC receptor protein (TR) and vitamin D receptor protein (VDR), the nuclear  
 CC acids encoding them and cells comprising them and a specified reporter  
 CC gene for the ligand dependent transcriptional factor. These proteins are  
 CC useful in the modulation of ligand dependent transcriptional factor  
 CC activity. The cells, mutant ERalpha and the polynucleotide encoding it  
 CC may be used in assays for qualitatively analysing an activity for  
 CC transactivation of a reporter gene by a test ERalpha, for screening  
 CC mutant ligand dependent transcriptional factors, for evaluating an  
 CC activity for transactivation of a reporter gene by a test ERalpha and/or  
 CC for screening a compound useful for treating a disorder of a mutant  
 CC ERalpha, especially breast cancer  
 XX  
 SQ Sequence 595 AA;  
 Query Match 99.2%; Score 1239.5; DB 4; Length 595;  
 Best Local Similarity 99.6%; Pred. No. 3.5e-124;  
 Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 Qy 1 SLALSLTADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINAKRV 60  
 Db 305 SLALSLTADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINAKRV 364  
 Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGVEI 120  
 Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGVEI 424  
 Qy 121 FDMLLATSSRRFMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEKDHHRVLDKITD 179  
 Db 425 FDMLLATSSRRFMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEKDHHRVLDKITD 484  
 Qy 180 TLHLMKAGLTTLQOQHRLAQLLLSHIRHMSNKGMEHLYSMKCNVVPVLYDLLEML 239  
 Db 485 TLHLMKAGLTTLQOQHRLAQLLLSHIRHMSNKGMEHLYSMKCNVVPVLYDLLEML 544  
 Qy 240 DAHLR 244  
 Db 545 DAHLR 549  
 RESULT 8  
 AAG84513  
 ID AAG84513 standard; protein; 595 AA.  
 XX  
 AC AAG84513;  
 XX  
 XX 10-SEP-2001 (first entry)  
 DE Human oestrogen receptor alpha protein mutant S578P.

XX Ligand dependent transcriptional factor; oestrogen receptor; ER;  
 KW glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;  
 KW MR; peroxisome proliferator-activated receptor protein; PPAR;  
 KW progesterone receptor protein; PR; pregnane X receptor protein; PXR;  
 KW thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;  
 KW transactivation; ERalpha; breast cancer; mutant; mutein.  
 XX Homo sapiens.  
 OS  
 XX WO200142307-A1.  
 PN  
 XX 14-JUN-2001.  
 XX  
 PD  
 XX  
 XX 01-DEC-2000; 2000WO-JP008553.  
 XX  
 XX 07-DEC-1999; 99JP-00348022.  
 PR 27-DEC-1999; 99JP-00370667.  
 PR 07-JUL-2000; 2000JP-00207011.  
 PR 21-JUL-2000; 2000JP-00220508.  
 PR 02-AUG-2000; 2000JP-00234053.  
 PR 03-AUG-2000; 2000JP-00235460.  
 PR 03-AUG-2000; 2000JP-00235461.  
 PR 03-AUG-2000; 2000JP-00235463.  
 XX (SUMO ) SUMITOMO CHEM CO LTD.  
 PA  
 XX Saito K, Ohe N, Satoh H;  
 XX WPI; 2001-367866/38.  
 XX  
 DR Ligand dependent transcriptional factors, nuclear acids encoding them and  
 XX cells comprising them and a specified reporter gene, useful for screening  
 XX agents for the treatment of breast cancer.  
 XX  
 PS Claim 20; Page 194-197; 276pp; English.  
 XX  
 CC The present invention relates to ligand dependent transcriptional factors  
 CC including oestrogen receptor (ER) alpha and beta protein, glucocorticoid  
 CC receptor protein (GR), mineralocorticoid receptor protein (MR),  
 CC peroxisome proliferator-activated receptor protein (PPAR), progesterone  
 CC receptor protein (PR), pregnane X receptor protein (PXR), thyroid hormone  
 CC receptor protein (TR) and vitamin D receptor protein (VDR), the nuclear  
 CC acids encoding them and cells comprising them and a specified reporter  
 CC gene for the ligand dependent transcriptional factor. These proteins are  
 CC useful in the modulation of ligand dependent transcriptional factor  
 CC activity. The cells, mutant ERalpha and the polynucleotide encoding it  
 CC may be used in assays for qualitatively analysing an activity for  
 CC transactivation of a reporter gene by a test ERalpha, for screening  
 CC mutant ligand dependent transcriptional factors, for evaluating an  
 CC activity for transactivation of a reporter gene by a test ERalpha and/or  
 CC for screening a compound useful for treating a disorder of a mutant  
 CC ERalpha, especially breast cancer  
 XX  
 SQ Sequence 595 AA;  
 Query Match 99.2%; Score 1239.5; DB 4; Length 595;  
 Best Local Similarity 99.6%; Pred. No. 3.5e-124;  
 Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 Qy 1 SLALSLTADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINAKRV 60  
 Db 305 SLALSLTADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINAKRV 364  
 Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGVEI 120  
 Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGVEI 424  
 Qy 121 FDMLLATSSRRFMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEKDHHRVLDKITD 179  
 Db 425 FDMLLATSSRRFMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEKDHHRVLDKITD 484  
 Qy 180 TLHLMKAGLTTLQOQHRLAQLLLSHIRHMSNKGMEHLYSMKCNVVPVLYDLLEML 239

Db 485 TLIHLMKAGLTQQQHQRQAQLLLILSHIRMSNKGMEHLYSMKCKNVVPLYDILLEML 544  
QY 240 DAHRL 244  
Db 545 DAHRL 549  
RESULT 9  
AAG84506  
ID AAG84506 standard; protein; 595 AA.  
AC AAG84506;  
XX  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Human oestrogen receptor alpha protein mutant K303R.  
XX  
XX Ligand dependent transcriptional factor; oestrogen receptor; ER;  
KW glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;  
KW NR; peroxisome proliferator-activated receptor protein; PPAR;  
KW progesterone receptor protein; PR; pregnane X receptor protein; PXR;  
KW thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;  
KW transactivation; ERalpha; breast cancer; mutant; mutein.  
XX  
OS Homo sapiens.  
XX  
XX WO200142307-A1.  
XX  
XX 14-JUN-2001.  
XX  
XX 01-DEC-2000; 2000WO-JP008553.  
XX  
XX 07-DEC-1999; 99JP-00348022.  
PR 27-DEC-1999; 99JP-00370667.  
PR 07-JUL-2000; 2000JP-00207011.  
PR 21-JUL-2000; 2000JP-00205058.  
PR 02-AUG-2000; 2000JP-00234053.  
PR 03-AUG-2000; 2000JP-00235460.  
PR 03-AUG-2000; 2000JP-00235461.  
PR 03-AUG-2000; 2000JP-00235463.  
XX  
XX (SUMO ) SUMITOMO CHEM CO LTD.  
XX  
XX Saito K, Ohe N, Satoh H;  
XX  
XX WPI; 2001-367866/38.  
XX  
XX ligand dependent transcriptional factors, nucleic acids encoding them and  
PT cells comprising them and a specified reporter gene, useful for screening  
PT agents for the treatment of breast cancer.  
XX  
XX Claim 15; Page 170-174; 276pp; English.  
XX  
XX The present invention relates to ligand dependent transcriptional factors  
CC including oestrogen receptor (ER) alpha and beta protein, glucocorticoid  
CC receptor protein (GR), mineralocorticoid receptor protein (MR),  
CC peroxisome proliferator-activated receptor protein (PPAR), progesterone  
CC receptor protein (PR), pregnane X receptor protein (PXR), thyroid hormone  
CC receptor protein (TR) and vitamin D receptor protein (VDR), the nucleic  
CC acids encoding them and cells comprising them and a specified reporter  
CC gene for the ligand dependent transcriptional factor. These proteins are  
CC useful in the modulation of ligand dependent transcriptional factor it  
CC activity. The cells, mutant ERalpha and the polynucleotide encoding it  
CC may be used in assays for qualitatively analysing an activity for  
CC transactivation of a reporter gene by a test ERalpha, for screening  
CC mutant ligand dependent transcriptional factors, for evaluating an  
CC activity for transactivation of a reporter gene by a test ERalpha and/or  
CC for screening a compound useful for treating a disorder of a mutant  
CC ERalpha, especially breast cancer  
XX  
XX Sequence 595 AA;

Query Match 99.2%; Score 1239.5; DB 4; Length 595;  
Best Local Similarity 99.6%; Pred. No. 3.5e-124;  
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 SLALSITADQWVSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
Db 305 SLALSITADQWVSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364  
QY 61 PGFVDTLTHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVSGMVEI 120  
Db 365 PGFVDTLTHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVSGMVEI 424  
QY 121 FDMLLATSSRRFRMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179  
Db 425 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484  
QY 180 TLIHLMKAGLTQQQHQRQAQLLLILSHIRMSNKGMEHLYSMKCKNVVPLYDILLEML 239  
Db 485 TLIHLMKAGLTQQQHQRQAQLLLILSHIRMSNKGMEHLYSMKCKNVVPLYDILLEML 544  
QY 240 DAHRL 244  
Db 545 DAHRL 549  
RESULT 10  
ABB76378  
ID ABB76378 standard; protein; 595 AA.  
XX  
AC ABB76378;  
XX  
DT 22-AUG-2002 (first entry)  
XX  
DE Human nuclear oestrogen receptor alpha.  
XX  
XX Oestrogen; receptor; human; transgenic mouse; cytostatic;  
KW antiinflammatory; antidiabetic; endocrine; anorectic; hepatotropic.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT Domain 180..262  
FT /note= "DNA-binding domain"  
FT Region 263..301  
FT /note= "D hinge region"  
FT Domain 302..552  
FT /note= "ligand-binding domain"  
XX  
XX WO200228175-A2.  
XX  
XX 11-APR-2002.  
XX  
XX 28-SEP-2001; 2001WO-IB002246.  
XX  
XX 03-OCT-2000; 2000FR-00012570.  
PR 11-MAY-2001; 2001US-00853033.  
XX  
XX (ADER-) ADEREGEM ASSOC DEV RECH EN GENETIQ.  
XX  
XX Chambon P, Metzger D;  
DR WPI; 2002-463217/49.  
XX N-PSDB; ABL57497.  
XX  
XX A transgenic mouse, useful in screening for medicaments for the treatment  
PT of e.g., diabetes or skin cancers, comprises a fusion protein between a  
PT recombinase Cre, and a modified ligand binding domain of the nuclear  
PT estrogen receptor alpha.  
XX  
XX Claim 6; Page 131-132; 149pp; English.  
XX  
XX The present sequence is the protein sequence of the human nuclear  
CC oestrogen receptor alpha (I). The invention relates to a non-human



metazoan organism, especially a transgenic mouse, characterised in that at least one cell comprises: (i) a fusion protein formed from a recombinase (Cre), a hinge region (preferably human (I) D hinge), and a modified ligand binding domain (LBD) of a nuclear oestrogen receptor, especially human (I), its fragment or variant; and (ii) one or more genes or DNA sequences of interest belonging to the genome of the organism, into which one or more recognition sites of the recombinase protein are inserted. The (I) LBD domain is preferably modified by a G521R, G400V, or M543A/I544A mutation. The fusion protein has negligible, or even zero, recombinase activity in the presence of a natural ligand such as oestradiol, but recombinase activity is induced by a small quantity of a synthetic ligand that has antioestrogenic activity, e.g. tamoxifen or 4-hydroxytamoxifen. The metazoan organism or its cells, such as epidermal cells, hepatocytes or adipocytes, are useful in carrying out a spatiotemporally controlled site-specific recombination of a DNA sequence of interest in its natural chromatin environment. It is also used in screening of medicaments for pathological conditions associated with an alteration of the expression and/or function of the DNA sequence of interest, such as skin cancer, inflammation, diabetes, alopecia, obesity, or in promoting hepatic regeneration

Query Match 99.2%; Score 1239.5; DB 5; Length 595;  
Best Local Similarity 99.6%; Pred. No. 3.5e-124;  
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
1 SLALSITADQWVSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINKRV 60  
305 SLALSITADQWVSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINKRV 364  
61 PGFVDLTLDHQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNGKCVGMEI 120  
365 PGFVDLTLDHQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNGKCVGMEI 424  
121 FDMLLATSRFRMNLQOG-BFVCLKSIILLNSGVYTFSLSTLSLEKDHHRVLDKID 179  
425 FDMLLATSRFRMNLQOG-BFVCLKSIILLNSGVYTFSLSTLSLEKDHHRVLDKID 484  
180 TLHLMAKAGLTQQOQHRLAQLLLSHIRHMSNGMEHLYSMKCKNVVPLDYLLEML 239  
485 TLHLMAKAGLTQQOQHRLAQLLLSHIRHMSNGMEHLYSMKCKNVVPLDYLLEML 544  
240 DAHRL 244  
545 DAHRL 549

ADP05661 standard; protein; 595 AA.  
ADP05661;  
26-AUG-2004 (first entry)  
Human nuclear receptor protein SeqID35.  
disease risk; disorder risk; mutation; polymorphism;  
nuclear receptor protein; antibacterial; antithyroid; cardiovascular-Gen;  
cytostatic; dermatological; eating-Disorders-Gen; gastrointestinal-Gen;  
gynaecological; hepatotropic; immunosuppressive; muscular-Gen;  
nephrotropic; osteopathic; virocid; adrenal gland; colon;  
cardiovascular; intestine; kidney; liver; lung; muscular; ovary; blood;  
prostate; skin; spleen; stomach; testes; thymus; thyroid; uterus;  
pancreas; bone; joint; breast; immune system; metabolic;  
nutritive disease; human.  
Homo sapiens.  
WO2004045369-A2.  
03-JUN-2004.

12-NOV-2003; 2003MO-US036229.  
14-NOV-2002; 2002US-0426305P.  
(NURA-) NURA INC.  
Gaitanaris GA, Bergmann JE, Gracero A, Hohmann J, Li F;  
Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;  
WPI; 2004-449627/42.  
N-PSDB; ADP05662.  
Determining an increased risk for e.g. colon, brain or breast disease or disorder, by detecting a mutation or polymorphism in the nuclear receptor gene, or measuring expression or biological activity level of the nuclear receptor.  
Claim 1; SEQ ID NO 35; 508pp; English.

This invention relates to a novel method of determining whether a patient has an increased risk for developing a disease or disorder which comprises determining the presence of a mutation or polymorphism in the patient's gene encoding a nuclear receptor protein or measuring the expression or level of biological activity of a nuclear receptor polypeptide in the patient or in a cell of the patient. The invention may be useful for the development of compounds with an antibacterial, antithyroid, cardiovascular-Gen, cytostatic, dermatological, eating-Disorders-Gen, gastrointestinal-Gen, gynaecological, hepatotropic, immunosuppressive, muscular-Gen, nephrotropic, osteopathic or virocid activity. The method is useful for determining whether a patient has an increased risk for developing a disease or disorder. The nucleic acid encoding a nuclear receptor polypeptide, an expression vector comprising the nucleic acid operably linked to a promoter, or a compound that modulates the biological activity of a nuclear receptor polypeptide, is useful for treating or preventing a disease or disorder of the adrenal gland, colon, cardiovascular, intestine, kidney, liver, lung, muscular, ovary, blood, prostate, skin, spleen, stomach, testes, thymus, thyroid, uterus, pancreas, bone and joints, breast, or immune system, or metabolic or nutritive disease or disorder. The present sequence is that of a nuclear receptor protein which may be used in the method of the invention.

Query Match 99.2%; Score 1239.5; DB 8; Length 595;  
Best Local Similarity 99.6%; Pred. No. 3.5e-124;  
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
1 SLALSITADQWVSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINKRV 60  
305 SLALSITADQWVSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINKRV 364  
61 PGFVDLTLDHQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNGKCVGMEI 120  
365 PGFVDLTLDHQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNGKCVGMEI 424  
121 FDMLLATSRFRMNLQOG-BFVCLKSIILLNSGVYTFSLSTLSLEKDHHRVLDKID 179  
425 FDMLLATSRFRMNLQOG-BFVCLKSIILLNSGVYTFSLSTLSLEKDHHRVLDKID 484  
180 TLHLMAKAGLTQQOQHRLAQLLLSHIRHMSNGMEHLYSMKCKNVVPLDYLLEML 239  
485 TLHLMAKAGLTQQOQHRLAQLLLSHIRHMSNGMEHLYSMKCKNVVPLDYLLEML 544  
240 DAHRL 244  
545 DAHRL 549  
RESULT 12  
ADO42788  
ID ADO42788 standard; protein; 595 AA.

XX ADO42788;  
 AC 26-AUG-2004 (first entry)  
 DT  
 DE Wild type human oestrogen receptor-alpha (ER) protein.  
 XX  
 KW human; oestrogen receptor-alpha; ER; ER activity regulator substance;  
 KW anti-oestrogen substance.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004046352-A1.  
 XX  
 PD 03-JUN-2004.  
 XX  
 PF 14-NOV-2003; 2003WO-JP014494.  
 XX  
 PR 15-NOV-2002; 2002JP-00331994.  
 PR 15-NOV-2002; 2002JP-00331995.  
 PR 15-NOV-2002; 2002JP-00331996.  
 XX  
 XX (SUMO ) SUMITOMO CHEM CO LTD.  
 PA  
 XX Fujimori K;  
 XX  
 PI WPI; 2004-431978/40.  
 XX  
 XX New mutant estrogen receptor-alpha useful for determining effectiveness  
 of treatment by estrogen receptor activity regulator substance and  
 PT antiestrogen substance.  
 PT  
 XX  
 PS Claim 1; SEQ ID NO 1; 111pp; Japanese.  
 XX  
 CC The invention comprises the amino acid sequences of mutant human  
 CC oestrogen receptor-alpha (ER) proteins. The mutant ER proteins of the  
 CC invention are useful for determining the effectiveness of a treatment by  
 CC an ER activity regulator substance, and for determining the effectiveness  
 CC of a treatment by an anti-oestrogen substance. The present amino acid  
 CC sequence represents the wild-type human ER protein.  
 XX  
 XX Sequence 595 AA;  
 SQ  
 Query Match 99.2%; Score 1239.5; DB 8; Length 595;  
 Best Local Similarity 99.6%; Pred. No. 3.5e-124;  
 Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 SLALSITADQWVSALLDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRV 60  
 DB 305 SLALSITADQWVSALLDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRV 364  
 QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEV 120  
 DB 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEV 424  
 QY 121 FDMILATSRFRMNLQGEFVCLSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179  
 DB 425 FDMILATSRFRMNLQGEFVCLSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484  
 QY 180 TLIIHMAKAGLTQQOQHRLAQLLLILSHIRMSNKGMEHLYSMCKCNVVPYDILLEML 239  
 DB 485 TLIIHMAKAGLTQQOQHRLAQLLLILSHIRMSNKGMEHLYSMCKCNVVPYDILLEML 544  
 QY 240 DAHRL 244  
 DB 545 DAHRL 549  
 RESULT 13  
 ADO42830  
 ID ADO42830 standard; protein; 595 AA.  
 XX  
 AC ADO42830;  
 XX

XX 26-AUG-2004 (first entry)  
 DT  
 DE Human oestrogen receptor-alpha (ER) protein.  
 XX  
 KW human; oestrogen receptor-alpha; ER; ER activity regulator substance;  
 KW anti-oestrogen substance.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004046352-A1.  
 XX  
 PD 03-JUN-2004.  
 XX  
 PF 14-NOV-2003; 2003WO-JP014494.  
 XX  
 PR 15-NOV-2002; 2002JP-00331994.  
 PR 15-NOV-2002; 2002JP-00331995.  
 PR 15-NOV-2002; 2002JP-00331996.  
 XX  
 XX (SUMO ) SUMITOMO CHEM CO LTD.  
 PA  
 XX Fujimori K;  
 XX  
 PI WPI; 2004-431978/40.  
 XX  
 XX New mutant estrogen receptor-alpha useful for determining effectiveness  
 of treatment by estrogen receptor activity regulator substance and  
 PT antiestrogen substance.  
 PT  
 XX  
 PS Disclosure; Fig 19; 111pp; Japanese.  
 XX  
 CC The invention comprises the amino acid sequences of mutant human  
 CC oestrogen receptor-alpha (ER) proteins. The mutant ER proteins of the  
 CC invention are useful for determining the effectiveness of a treatment by  
 CC an ER activity regulator substance, and for determining the effectiveness  
 CC of a treatment by an anti-oestrogen substance. The present amino acid  
 CC sequence represents a human ER protein.  
 XX  
 XX Sequence 595 AA;  
 SQ  
 Query Match 99.2%; Score 1239.5; DB 8; Length 595;  
 Best Local Similarity 99.6%; Pred. No. 3.5e-124;  
 Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 SLALSITADQWVSALLDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRV 60  
 DB 305 SLALSITADQWVSALLDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRV 364  
 QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEV 120  
 DB 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEV 424  
 QY 121 FDMILATSRFRMNLQGEFVCLSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179  
 DB 425 FDMILATSRFRMNLQGEFVCLSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484  
 QY 180 TLIIHMAKAGLTQQOQHRLAQLLLILSHIRMSNKGMEHLYSMCKCNVVPYDILLEML 239  
 DB 485 TLIIHMAKAGLTQQOQHRLAQLLLILSHIRMSNKGMEHLYSMCKCNVVPYDILLEML 544  
 QY 240 DAHRL 244  
 DB 545 DAHRL 549  
 RESULT 14  
 AAB26784  
 ID AAB26784 standard; protein; 244 AA.  
 XX  
 AC AAB26784;  
 XX  
 DT 18-JAN-2001 (first entry)

XX Oestrogen receptor protein sequence.

DE Homology model; ligand binding domain; glucocorticoid receptor; AIDS; 179

KW hypertension; diabetes; obesity; glaucoma; depression; wound; 180

KW protein co-ordinate data; thyroid hormone receptor; oestrogen receptor. 239

XX Unidentified. 240

XX WO200052050-A2. 241

XX 08-SEP-2000. 242

XX 01-MAR-2000; 2000WO-GB000727. 243

XX 01-MAR-1999; 99GB-00004441. 244

XX 22-APR-1999; 99GB-00009151. 245

XX (KARO-) KARO BIO AB. 246

XX Gillner M, Greenidge P; 247

XX WPI; 2000-549565/50. 248

XX Designing a homology model of the ligand binding domain of a 249

XX glucocorticoid receptor displayed as a three-dimensional image, useful 250

XX for identifying agonists and antagonists for treating e.g. inflammation, 251

XX hypertension, glaucoma, diabetes. 252

XX Disclosure; Fig 6; 246pp; English. 253

XX This invention relates to a method for designing an homology model of the 254

XX ligand binding domain of a glucocorticoid receptor. The homology model 255

XX may be displayed as a three-dimensional image. The method comprises: (a) 256

XX providing an amino acid sequence and an x-ray crystallographic structure 257

XX of the ligand binding domain of a thyroid, oestrogen or progesterone 258

XX receptor; (b) modifying the x-ray crystallographic structure to take 259

XX account of differences between the amino acid configuration of the ligand 260

XX binding domain of the glucocorticoid receptor and the thyroid, oestrogen, 261

XX or progesterone receptor; (c) verifying the accuracy of the homology 262

XX model by comparing it with experimentally-determined binding properties 263

XX of a number of ligands for the glucocorticoid receptor; and (d) modifying 264

XX the homology model for greater consistency with the binding properties. 265

XX The homology model is useful for drug screening and designing ligands 266

XX (agonists and antagonists) capable of binding to a glucocorticoid 267

XX receptor. The identified agonists are useful for the treatment of 268

XX inflammation and also in immunosuppressive therapy. The identified 269

XX antagonists are useful for the treatment of hypertension, diabetes, 270

XX obesity, glaucoma, depression, acquired immune deficiency syndrome (AIDS) 271

XX and wounds. The homology models are also useful for electronic screening 272

XX of compound databases, de novo drug design and/or prediction of binding 273

XX affinities of glucocorticoid receptor ligands for the receptor by 274

XX Sequence 244 AA;

Query Match 98.8%; Score 1235.5; DB 3; Length 244;

Best Local Similarity 99.6%; Pred. No. 2.8e-124;

Matches 243; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SLALSTADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMNAKRV 60

DB 1 SLALSTADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMNAKRV 60

QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGWEI 120

DB 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGWEI 120

QY 121 FDMLLATSSRRFMNLOQ-EFVCLKSIILLNSGVYTFLLSKSLSEKDHHRVLDKITD 179

DB 121 FDMLLATSSRRFMNLOQGEFVCLKSIILLNSGVYTFLLSKSLSEKDHHRVLDKITD 180

QY 180 TLIIHMAKAGITLQOQHQAQLLLIILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLML 239

DB 181 TLIIHMAKAGITLQOQHQAQLLLIILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLLLML 240

QY 240 DAHR 243

DB 241 DAHR 244

RESULT 15

AAB26780

ID AAB26780 standard; protein; 244 AA.

XX AAB26780;

XX 18-JAN-2001 (first entry)

XX Human oestrogen receptor protein sequence.

XX Homology model; ligand binding domain; glucocorticoid receptor; AIDS; 245

XX hypertension; diabetes; obesity; glaucoma; depression; wound; human; 246

XX protein co-ordinate data; thyroid hormone receptor; oestrogen receptor. 247

XX Homo sapiens.

XX WO200052050-A2.

XX 08-SEP-2000.

XX 01-MAR-2000; 2000WO-GB000727.

XX 01-MAR-1999; 99GB-00004441.

XX 22-APR-1999; 99GB-00009151.

XX (KARO-) KARO BIO AB.

XX Gillner M, Greenidge P;

XX WPI; 2000-549565/50.

XX Designing a homology model of the ligand binding domain of a 245

XX glucocorticoid receptor displayed as a three-dimensional image, useful 246

XX for identifying agonists and antagonists for treating e.g. inflammation, 247

XX hypertension, glaucoma, diabetes. 248

XX Disclosure; Fig 2A; 246pp; English. 249

XX This invention relates to a method for designing an homology model of the 250

XX ligand binding domain of a glucocorticoid receptor. The homology model 251

XX may be displayed as a three-dimensional image. The method comprises: (a) 252

XX providing an amino acid sequence and an x-ray crystallographic structure 253

XX of the ligand binding domain of a thyroid, oestrogen or progesterone 254

XX receptor; (b) modifying the x-ray crystallographic structure to take 255

XX account of differences between the amino acid configuration of the ligand 256

XX binding domain of the glucocorticoid receptor and the thyroid, oestrogen, 257

XX or progesterone receptor; (c) verifying the accuracy of the homology 258

XX model by comparing it with experimentally-determined binding properties 259

XX of a number of ligands for the glucocorticoid receptor; and (d) modifying 260

XX the homology model for greater consistency with the binding properties. 261

XX The homology model is useful for drug screening and designing ligands 262

XX (agonists and antagonists) capable of binding to a glucocorticoid 263

XX receptor. The identified agonists are useful for the treatment of 264

XX inflammation and also in immunosuppressive therapy. The identified 265

XX antagonists are useful for the treatment of hypertension, diabetes, 266

XX obesity, glaucoma, depression, acquired immune deficiency syndrome (AIDS) 267

XX and wounds. The homology models are also useful for electronic screening 268

XX of compound databases, de novo drug design and/or prediction of binding 269

XX affinities of glucocorticoid receptor ligands for the receptor by 270

CC molecular mechanics scoring functions. The specification contains protein  
CC co-ordinate data for the glucocorticoid receptor models produced using  
CC the method, based on the X-ray crystallographic structure of the  
CC oestrogen and progesterone receptors. The present sequence represents the  
CC human oestrogen receptor protein. The protein is used in an example of  
CC the method of the invention for homology modelling based on the thyroid  
CC receptor  
XX  
SQ Sequence 244 AA;

Query Match 98.8%; Score 1235.5; DB 3; Length 244;  
Best Local Similarity 99.6%; Pred. No. 2.8e-124;  
Matches 243; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 SLALSITADQMVSALDAPPPILYSEYDPTRPSPSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 1 SLALSITADQMVSALDAPPPILYSEYDPTRPSPSEASMMGLLTNLADRELVHMINWAKRV 60  
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLPAPNLLIDRNQKCGVEGMVEI 120  
DB 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLPAPNLLIDRNQKCGVEGMVEI 120  
QY 121 FDMLLATSSRFRMMNIQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179  
DB 121 FDMLLATSSRFRMMNIQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 180  
QY 180 TLHLMAKAGLTQQOQHRLAQILLILSHIRMSNKGMEHLYSMCKKNVPLYDILLEML 239  
DB 181 TLHLMAKAGLTQQOQHRLAQILLILSHIRMSNKGMEHLYSMCKKNVPLYDILLEML 240  
QY 240 DAHR 243  
DB 241 DAHR 244

Search completed: November 8, 2004, 08:26:23  
Job time : 60.7592 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2004, 08:05:27 ; Search time 45:1837 Seconds  
(without alignments)  
3132.595 Million cell updates/sec

Title: US-09-830-693B-28

Perfect score: 1230

Sequence: 1 SLALSLTADQMSALLDAEP.....CKNVVPLYLLEMLDAHRL 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1206.5	98.1	595	1	ESR1_HUMAN
2	1175.5	95.6	596	2	Q6Q1S5
3	1175.5	95.6	596	2	AAS46251
4	1171.5	95.2	599	1	ESR1_MOUSE
5	1167.5	94.9	600	1	ESR1_RAT
6	1164.5	94.7	595	1	ESR1_PIG
7	1159.5	94.3	595	1	ESR1_MESAU
8	1146.5	93.2	587	2	Q8UWB0
9	1146.5	93.2	594	1	ESR1_HORSE
10	1144.5	93.0	587	1	ESR1_PORGU
11	1143.5	93.0	589	1	ESR1_CHICK
12	1142.5	92.9	587	2	Q765N7
13	1142.5	92.9	587	2	BAD08348
14	1139.5	92.6	589	2	Q8AYH0
15	1137.5	92.5	353	2	Q8CGK8
16	1137.5	92.5	431	2	Q95L13
17	1110.5	90.3	581	2	Q8UWA9
18	1103.5	89.7	349	1	ESR1_ANOCA
19	1042.5	84.8	427	2	Q6W5G5
20	1042.5	84.8	427	2	QAQ84784
21	1042.5	84.8	543	2	Q6W5G9
22	1042.5	84.8	543	2	QAQ84780
23	1042.5	84.8	585	2	Q6W5G7
24	1042.5	84.8	585	2	QAQ84782
25	1037.5	84.3	586	1	ESR1_XENLA
26	1033.5	84.0	427	2	Q6W5G6
27	1033.5	84.0	427	2	QAQ84783
28	992.5	80.7	307	1	ESR1_CNEUN
29	830	67.5	542	2	Q90Z56
30	828.5	67.4	174	1	ESR1_BOVIN
31	811.5	66.0	570	2	Q800Q2

Q9ddz4 micropterus  
Aa44622 micropterus  
Q7c2k8 halichoeres  
Q7az10 fundulus he  
Q42132 pagrus majo  
P57753 micropogoni  
Q9pv29 sparus aura  
P50241 oryzias lat  
Q804q6 acanthopagr  
Q6mzg9 homo sapien  
Cae45369 homo sapi  
P16058 oncorhynchus  
Q9yh33 oreochromis

32 808.5 65.7 627 2 Q9DDZ4  
33 808.5 65.7 627 2 AAG44622  
34 806.5 65.6 574 2 Q7T2K8  
35 799.5 65.0 620 2 Q7SZ10  
36 797.5 64.8 581 1 ESR1\_PAGNA  
37 796.5 64.8 525 1 ESR1\_MICUN  
38 794.5 64.6 579 1 ESR1\_SPAU  
39 792.5 64.4 620 1 ESR1\_ORYLA  
40 789.5 64.2 583 2 Q804Q6  
41 789 64.1 310 2 Q6MZ09  
42 789 64.1 310 2 CAE45369  
43 786 63.9 578 2 Q8QHL0  
44 785.5 63.9 622 1 ESR1\_ONCMY  
45 784.5 63.8 585 1 ESR1\_ORENI

## ALIGNMENTS

RESULT 1  
ESR1\_HUMAN STANDARD; PRT; 595 AA.  
AC P03372; Q13511; Q14276; Q9NU51; Q9UDZ7; Q9UIS7;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Estrogen receptor (ER) (Estadiol receptor) (ER-alpha).  
GN Name=ESR1; Synonyms=NR3A1, ESR;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A. (ISOFORM LONG).  
RX MEDLINE=86122927; PubMed=3753802;  
RA Greene G.L., Gilna P., Waterfield M., Baker A., Hort Y., Shine J.;  
RT "Sequence and expression of human estrogen receptor complementary  
RT DNA.";  
RL Science 231:1150-1154 (1986).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM LONG).  
RX MEDLINE=86146892; PubMed=3754034;  
RA Green S., Walter P., Kumar V., Krust A., Bornert J.-M., Argos P.,  
RA Chambon P.;  
RT "Human oestrogen receptor cDNA: sequence, expression and homology to  
RT v-erb-A.";  
RL Nature 320:134-139 (1986).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANT ASP-411 INS.  
RC TISSUE=Breast;  
RX MEDLINE=96174665; PubMed=8600466;  
RA Pink J.J., Wu S.Q., Wolf D.M., Billmor M.M., Jordan V.C.;  
RT "A novel 80 kDa human estrogen receptor containing a duplication of  
RT exons 6 and 7.";  
RL Nucleic Acids Res. 24:962-969 (1996).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM LONG), AND VARIANT SER-77.  
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,  
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,  
RA Schackwitz W.S., Sherwood J.K., Wittrak L.A., Nickerson D.A.;  
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department  
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu.);  
RT Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 152-595 FROM N.A. (ISOFORM LONG).  
RX MEDLINE=20084372; PubMed=10619354;  
RA Schubert E.L., Lee M.K., Newman B., King M.C.;  
RT "Single nucleotide polymorphisms (SNPs) in the estrogen receptor gene  
RT and breast cancer susceptibility.";  
RL J. Steroid Biochem. Mol. Biol. 71:21-27 (1999).  
RN [6]  
RP SEQUENCE OF 216-434 FROM N.A., AND ALTERNATIVE SPLICING.  
RC TISSUE=Breast carcinoma;

RX MEDLINE=93153765; PubMed=7916651;  
RA Pfeiffer U., Fecarotta E., Castagnetta L., Vidali G.;  
RT "Estrogen receptor variant messenger RNA lacking exon 4 in estrogen-  
responsive human breast cancer cell lines.";   
RN Cancer Res. 53:741-743(1993).  
RN [7]  
RP SEQUENCE OF 110-117, PHOSPHORYLATION, AND MUTAGENESIS.  
RX MEDLINE=96026869; PubMed=7476978;  
RA Joel P.B., Traish A.M., Lannigan D.A.;  
RT "Estradiol and phorbol ester cause phosphorylation of serine 118 in  
the human estrogen receptor.";   
RN Mol. Endocrinol. 9:1041-1052(1995).  
RN [8]  
RP SEQUENCE OF 354-548 FROM N.A.  
RC TISSUE=Breast carcinoma;  
RA Naundorf H., Becker M., Fiebig C., Buettner B., Fichtner I.;  
RT "Mechanisms of acquired tamoxifen resistance in a xenotransplanted  
human breast carcinoma.";   
RN Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP SEQUENCE OF 413-595 FROM N.A.  
RA Arker A.;  
RN Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE OF 532-542, AND PHOSPHORYLATION.  
RX MEDLINE=95280953; PubMed=7539106;  
RA Arnold S.F., Obourn J.D., Jaffe H., Notides A.C.;  
RT "Phosphorylation of the human estrogen receptor on tyrosine 537 in  
vivo and by src family tyrosine kinases in vitro.";   
RN Mol. Endocrinol. 9:24-33(1995).  
RN [11]  
RP INTERACTION WITH NCOA6.  
RX MEDLINE=20036574; PubMed=10567404;  
RA Lee S.-K., Anzick S.L., Choi J.-E., Bubendorf L., Guan X.-Y.,  
Jung Y.-K., Kallioniemi O.P., Kononen J., Trent J.M., Azorsa D.,  
Jhun B.-H., Cheong J.H., Lee Y.C., Meltzer P.S., Lee J.W.;  
RT "A nuclear factor ASC-2, as a cancer-amplified transcriptional  
coactivator essential for ligand-dependent transactivation by nuclear  
receptors in vivo.";   
RN J. Biol. Chem. 274:34283-34293(1999).  
RN [12]  
RP INTERACTION WITH NCOA5.  
RX MEDLINE=20565767; PubMed=11113208; DOI=10.1128/MCB.21.1.343-353.2001;  
RA Sauve F., McBroom L.D.B., Gallant J., Moraitis A.N., Labrie F.,  
Giguere V.;  
RT "CIA, a novel estrogen receptor coactivator with a bifunctional  
nuclear receptor interacting determinant.";   
RN Mol. Cell. Biol. 21:343-353(2001).  
RN [13]  
RP PHOSPHORYLATION.  
RX MEDLINE=95140025; PubMed=7838153;  
RA Arnold S.F., Obourn J.D., Jaffe H., Notides A.C.;  
RT "Serine 167 is the major estradiol-induced phosphorylation site on the  
human estrogen receptor.";   
RN Mol. Endocrinol. 8:1208-1214(1994).  
RN [14]  
RP PHOSPHORYLATION SITES SER-104 AND SER-106, AND MUTAGENESIS.  
RX MEDLINE=99357754; PubMed=10428798;  
RA Rogatsky I., Trowbridge J.M., Garabedian M.J.;  
RT "Potentiation of human estrogen receptor alpha transcriptional  
activation through phosphorylation of serines 104 and 106 by the  
cyclin A-CDK2 complex.";   
RN J. Biol. Chem. 274:22296-22302(1999).  
RN [15]  
RP STRUCTURE BY NMR OF 180-262.  
RX MEDLINE=91061891; PubMed=2247153;  
RA Schwabe J.W.E., Neuhaus D., Rhodes D.;  
RT "Solution structure of the DNA-binding domain of the oestrogen  
receptor.";   
RN Nature 348:458-461(1990).  
RN [16]  
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 180-262.  
RX MEDLINE=94037103; PubMed=8221895;

RA Schwabe J.W.E., Chapman L., Finch J.T., Rhodes D.;  
RT "The crystal structure of the estrogen receptor DNA-binding domain  
bound to DNA: how receptors discriminate between their response  
elements.";   
RN Cell 75:567-578(1993).  
RN [17]  
RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF 305-548.  
RX MEDLINE=97478539; PubMed=9338790;  
RA Brzowski A.M., Pike A.C.W., Dauter Z., Hubbard R.E., Bonn T.,  
Engstrom O., Oelman L., Greene G.L., Gustafsson J.-A., Carlquist M.;  
RT "Molecular basis of agonism and antagonism in the oestrogen  
receptor.";   
RN Nature 389:753-758(1997).  
RN [18]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 306-544.  
RX MEDLINE=98263297; PubMed=9600906;  
RA Tanenbaum D.M., Wang Y., Williams S.P., Sigler P.B.;  
RT "Crystallographic comparison of the estrogen and progesterone  
receptor's ligand binding domains.";   
RN Proc. Natl. Acad. Sci. U.S.A. 95:5998-6003(1998).  
RN [19]  
RP X-RAY CRYSTALLOGRAPHY (1.90 ANGSTROMS) OF 294-554.  
RX MEDLINE=99091051; PubMed=9875847;  
RA Shiao A.K., Barstad D., Loria P.M., Cheng L., Kushner P.J.,  
Agard D.A., Greene G.L.;  
RT "The structural basis of estrogen receptor/coactivator recognition and  
the antagonism of this interaction by tamoxifen.";   
RN Cell 95:927-937(1998).  
RN [20]  
RP 3D-STRUCTURE MODELING OF 311-547.  
RX MEDLINE=98280806; PubMed=9619507;  
RA Maalouf G.J., Xu W., Smith T., Mohr S.C.;  
RT "Homology model for the ligand-binding domain of the human estrogen  
receptor.";   
RN J. Biomol. Struct. Dyn. 15:841-850(1998).  
RN [21]  
RP VARIANT VAL-400.  
RX MEDLINE=9005402; PubMed=2792078;  
RA Tori L., Mullick A., Metzger D., Ponglikitmongkol M., Park I.,  
Chambon P.;  
RT "The cloned human oestrogen receptor contains a mutation which alters  
its hormone binding properties.";   
RN EMBO J. 8:1981-1986(1989).  
RN [22]  
RP VARIANT ALA-447.  
RX MEDLINE=92250650; PubMed=1577818;  
RA Reese J.C., Katzenellenbogen B.S.;  
RT "Characterization of a temperature-sensitive mutation in the hormone  
binding domain of the human estrogen receptor. Studies in cell  
extracts and intact cells and their implications for hormone-dependent  
transcriptional activation.";   
RN J. Biol. Chem. 267:9868-9873(1992).  
RN [23]  
RP VARIANT GLU-364.  
RX MEDLINE=97120591; PubMed=8961262;  
RA McInerney E.M., Ince B.A., Shapiro D.J., Katzenellenbogen B.S.;  
RT "A transcriptionally active estrogen receptor mutant is a novel type  
of dominant negative inhibitor of estrogen action.";   
RN Mol. Endocrinol. 10:1519-1526(1996).  
RN [24]  
RP VARIANT CYS-160.  
RX MEDLINE=97338667; PubMed=9195227;  
RA Anderson T.I., Wooster R., Laake K., Collins N., Warren W., Skrede M.,  
Beles R., Tveit K.M., Johnston S.R.D., Dowsett M., Olsen A.O.,  
Moeller P., Stratton M.R., Boerresen-Dale A.-L.;  
RT "Screening for ESR mutations in breast and ovarian cancer patients.";   
RN Hum. Mutat. 9:531-536(1997).  
RN CC -!- FUNCTION: Nuclear hormone receptor. The steroid hormones and their  
receptors are involved in the regulation of eukaryotic gene  
expression and affect cellular proliferation and differentiation  
in target tissues.  
RN CC -!- SUBUNIT: Binds DNA as a homodimer. Binds UBE1C (By similarity).  
RN CC Can form a heterodimer with ESR2. Interacts with NCOA3, NCOA5 and

CC NCOA6 coactivators, leading to a strong increase of transcription  
 CC of target genes.

Query Match 98.1%; Score 1206.5; DB 1; Length 595;  
 Best Local Similarity 96.3%; Pred. No. 1.8e-109;  
 Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 1 SLALSLTADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
 Db 305 SLALSLTADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364

Qy 61 PGFVDLTLDHVDVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEVEI 120  
 Db 365 PGFVDLTLDHVDVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEVEI 424

Qy 121 FDMLLATSSFRMNMNLOGEFVCLKSIILLNSGVYTFXXXXXXXREKDHHRVLDKIT 180  
 Db 425 FDMLLATSSFRMNMNLOGEFVCLKSIILLNSGVYTF-LSTLSLEKDHHRVLDKIT 483

Qy 181 DTLHLMAKAGLTQQOQHRLAQQLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDILLEM 240  
 Db 484 DTLHLMAKAGLTQQOQHRLAQQLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDILLEM 543

Qy 241 LDAHRL 246  
 Db 544 LDAHRL 549

RESULT 2  
 Q6Q1S5 PRELIMINARY; PRT; 596 AA.

ID Q6Q1S5  
 AC Q6Q1S5  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Estrogen receptor alpha.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RA Nishimura N., Tetsuka M.;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR000536; Hmon\_recept\_lig.  
 DR InterPro; IPR001292; Oestrgn\_receptor.  
 DR InterPro; IPR001723; Stdhmn\_receptor.  
 DR InterPro; IPR008946; Str\_ncl\_receptor.  
 DR InterPro; IPR001628; Znf\_C4steroid.  
 DR Pfam; PF00104; Hormone\_recep; 1.  
 DR Pfam; PF02159; Oest\_recep; 1.  
 DR Pfam; PF00105; Zf-C4; 1.  
 DR PRINTS; PR00543; OESTROGENR.  
 DR PRINTS; PR00398; STRDHOMONER.  
 DR PRINTS; PR00047; STROIDFINGER.  
 DR ProDom; PD000035; Znf\_C4steroid; 1.  
 DR SMART; SM00430; HOLI; 1.  
 DR SMART; SM00399; Znf\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
 KW DNA-binding; Metal-binding; Nuclear protein; Receptor;  
 KW Transcription regulation; Zinc; Zinc-finger.  
 SQ SEQUENCE 596 AA; 66489 MW; 3E2CE85BE7844FF2 CRC64;

Query Match 95.6%; Score 1175.5; DB 2; Length 596;  
 Best Local Similarity 93.1%; Pred. No. 2e-106;  
 Matches 229; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

ESR1\_MOUSE STANDARD; PRT; 599 AA.  
 ID ESR1\_MOUSE  
 AC P19785; Q9JUT5; Q9QY51; Q9QY52;  
 DT 01-FEB-1991 (Rel. 17, Created)

Qy 1 SLALSLTADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
 Db 306 SPVLSTADQMISALLEAPPIIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 365

Qy 61 PGFVDLTLDHVDVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEVEI 120  
 Db 366 PGFVDLTLDHVDVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEVEI 425

Qy 121 FDMLLATSSFRMNMNLOGEFVCLKSIILLNSGVYTFXXXXXXXREKDHHRVLDKIT 180  
 Db 426 FDMLLATSSFRMNMNLOGEFVCLKSIILLNSGVYTF-LSTLSLEKDHHRVLDKIT 484

Qy 181 DTLHLMAKAGLTQQOQHRLAQQLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDILLEM 240  
 Db 485 DTLHLMAKAGLTQQOQHRLAQQLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDILLEM 544

Qy 241 LDAHRL 246  
 Db 545 LDAHRL 550

RESULT 3  
 AAS46251 PRELIMINARY; PRT; 596 AA.

ID AAS46251  
 AC AAS46251  
 DT 03-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 03-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 03-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Estrogen receptor alpha.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RA Nishimura N., Tetsuka M.;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY538775; AAS46251.1; -.  
 KW Receptor.  
 SQ SEQUENCE 596 AA; 66489 MW; 3E2CE85BE7844FF2 CRC64;

Query Match 95.6%; Score 1175.5; DB 2; Length 596;  
 Best Local Similarity 93.1%; Pred. No. 2e-106;  
 Matches 229; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

Qy 1 SLALSLTADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
 Db 306 SPVLSTADQMISALLEAPPIIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 365

Qy 61 PGFVDLTLDHVDVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEVEI 120  
 Db 366 PGFVDLTLDHVDVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEVEI 425

Qy 121 FDMLLATSSFRMNMNLOGEFVCLKSIILLNSGVYTFXXXXXXXREKDHHRVLDKIT 180  
 Db 426 FDMLLATSSFRMNMNLOGEFVCLKSIILLNSGVYTF-LSTLSLEKDHHRVLDKIT 484

Qy 181 DTLHLMAKAGLTQQOQHRLAQQLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDILLEM 240  
 Db 485 DTLHLMAKAGLTQQOQHRLAQQLLILSHIRHMSNKGMEHLYSMCKKNVVPVLYDILLEM 544

Qy 241 LDAHRL 246  
 Db 545 LDAHRL 550

RESULT 4  
 ESR1\_MOUSE STANDARD; PRT; 599 AA.  
 ID ESR1\_MOUSE  
 AC P19785; Q9JUT5; Q9QY51; Q9QY52;  
 DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (rel. 17, last sequence update)  
DT 01-OCT-2004 (rel. 45, last annotation update)  
DE Estrogen receptor (ER) (Estrogen receptor) (ER-alpha).  
GN Name=ESR1; Synonyms=NR3a1, ESR, Estr, Estra;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Uterus;  
RX MEDLINE=91042558; PubMed=2484714;  
RA White R., Lees J.A., Needham M., Ham J., Parker M.;  
RT "Structural organization and expression of the mouse estrogen  
RL receptor.";  
RL Mol. Endocrinol. 1:735-744 (1987).  
RN [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Bone, and Thymus;  
RX MEDLINE=C57BL/6J; PubMed=12466851; DOI=10.1038/nature01266;  
RA Takaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Yikado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Gorkik A., Gough J.,  
RA Grimmond S., Gustinch S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Malcais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RL 20,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
RN [3]  
RN SEQUENCE OF 1-22 FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=20359284; PubMed=10899303;  
RA Kos M., O'Brien S., Flouriot G., Gannon F.;  
RT "Tissue-specific expression of multiple mRNA variants of the mouse  
RL estrogen receptor alpha gene.";  
RL FEBS Lett. 477:15-20 (2000).  
RN [4]  
RN SEQUENCE OF 269-599 FROM N.A.  
RC STRAIN=SJL/J, and B10.S/J; TISSUE=Spleen;  
RA Ma R.Z., Teuscher C.;  
RT "Screening for candidate genes of mouse autoimmune diseases.";  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RN CARBOHYDRATE-LINKAGE SITE SER-575.  
RX MEDLINE=97153020; PubMed=8999954;  
RA Jiang M.S., Hart G.W.;  
RT "A subpopulation of estrogen receptors are modified by O-linked N-  
RL acetylglucosamine.";  
RL J. Biol. Chem. 272:2421-2428 (1997).  
RN [6]  
RN CARBOHYDRATE-LINKAGE SITES SER-10; THR-50 AND SER-575.  
RX MEDLINE=21124487; PubMed=11226831;  
Cheng X., Hart G.W.;  
RT "Glycosylation of the murine estrogen receptor-alpha.";  
RL J. Steroid Biochem. Mol. Biol. 75:147-158 (2000).  
RN [7]  
RN INTERACTION WITH NCOA3.  
RX MEDLINE=97336097; PubMed=9192892;  
RA Torchia J., Rose D.W., Inostroza J., Kamei Y., Westin S., Glass C.K.,  
RA Rosenfeld M.G.;  
RT "The transcriptional co-activator p/CIP binds CBP and mediates  
RL nuclear-receptor function.";  
RL Nature 387:677-684 (1997).  
RN [8]  
RN INTERACTION WITH NCOA6.  
RX MEDLINE=20250907; PubMed=10789465;  
RA Zhu Y.-J., Kan L., Qi C., Kanwar Y.S., Yeldandi A.V., Rao M.S.,  
RA Reddy J.K.;  
RT "Isolation and characterization of peroxisome proliferator-activated  
RL receptor (PPAR) interacting protein (PRIP) as a coactivator for  
RT PPAR.";  
RL J. Biol. Chem. 275:13510-13516 (2000).  
CC -!- FUNCTION: Nuclear hormone receptor. The steroid hormones and their  
CC receptors are involved in the regulation of eukaryotic gene  
CC expression and affect cellular proliferation and differentiation  
CC in target tissues.  
CC -!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with  
CC ESR2. Interacts with NCOA3 and NCOA6 coactivators, leading to a  
CC strong increase of transcription of target genes. Interacts with  
CC NCOA5. Binds UBE1C (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,  
CC a DNA-binding domain and a C-terminal steroid-binding domain.  
CC -!- PTM: Phosphorylated by cyclin A/CDK2 (By similarity).  
CC -!- MISCELLANEOUS: In the absence of ligand, steroid hormone receptors  
CC are thought to be weakly associated with nuclear components;  
CC hormone binding greatly increases receptor affinity. The hormone-  
CC receptor complex appears to recognize discrete DNA sequences  
CC upstream of transcriptional start sites.  
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3  
CC subfamily.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
DR EMBL; M38651; AAA37580.1; -;  
DR EMBL; AK036627; BAC29510.1; -;  
DR EMBL; AK041525; BAC30973.1; -;  
DR EMBL; AJ276597; CAB85618.1; -;  
DR EMBL; AF128221; AAF22562.1; -;  
DR EMBL; AF128220; AAF22561.1; -;  
DR PIR; A40061; ORMSE.  
DR HSSP; P03372; IHCP.  
DR TRANSFAC; T00259; -;  
DR GlycoSuiteDB; P19785; -;  
DR MGD; MGI:1352467; ESR1.  
DR GO; GO:0016585; C:chromatin remodeling complex; ISS.  
DR GO; GO:0005737; C:cycloplasm; IDA.  
DR GO; GO:0016020; C:membrane; ISS.  
DR GO; GO:0005634; C:nucleus; IDA.  
DR GO; GO:0030284; F:estrogen receptor activity; ISS.  
DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; ISS.  
DR GO; GO:0016049; P:cell growth; NAS.  
DR GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.  
DR GO; GO:0045839; P:negative regulation of mitosis; NAS.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.  
DR InterPro; IPR000536; Hrmn\_recept\_lig.  
DR InterPro; IPR001292; Oestrgn\_receptor.  
DR InterPro; IPR001723; Stdhrmn\_receptor.  
DR InterPro; IPR008946; Str\_ncl\_receptor.



DR InterPro; IPR001628; Znf\_C4steroid.  
 DR Pfam; PF00104; Hormone\_recep; 1.  
 DR Pfam; PF02159; Oest\_recep; 1.  
 DR Pfam; PF00105; zf-C4; 1.  
 DR PRINTS; PR00543; OESTROGENR.  
 DR PRINTS; PR00398; STRDHORMONER.  
 DR PRINTS; PR00047; STROIDFINGER.  
 DR PRODOM; PD000035; Znf\_C4steroid; 1.  
 DR SMART; SM00430; HOLI; 1.  
 DR SMART; SM00399; Znf\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
 DR DNA-binding; Glycoprotein; Nuclear protein; Phosphorylation; Receptor;  
 KW Steroid-binding; Transcription regulation; Zinc-finger.  
 FT DOMAIN 1 188  
 FT DNAS BIND 189 254  
 FT ZN\_FING 189 209  
 FT ZN\_FING 225 249  
 FT DOMAIN 255 314  
 FT DOMAIN 315 599  
 FT DOMAIN 64 72  
 FT MOD\_RES 108 108  
 FT MOD\_RES 110 110  
 FT MOD\_RES 122 122  
 FT MOD\_RES 171 171  
 FT MOD\_RES 541 541  
 FT CARBOHYD 10 10  
 FT CARBOHYD 50 50  
 FT CARBOHYD 575 575  
 FT VARIANT 591 591  
 FT CONFLICT 269 269  
 FT SEQUENCE 599 AA; 66955 MW; 05F5B2FC21CC0A8B CRC64;  
 Query Match 95.2%; Score 1171.5; DB 1; Length 599;  
 Best Local Similarity 93.1%; Pred. No. 4.9e-106;  
 Matches 229; Conservative 5; Mismatches 11; Indels 1; Gaps 1;  
 QY 1 SLALSLTADQVMSALLDAEPILYSEYDPTPFSEASMGMLTLNADRELVHMINAKRV 60  
 DB 309 SPALSLTADQVMSALLDAEPIMYSEYDPTPFSEASMGMLTLNADRELVHMINAKRV 368  
 QY 61 PGFVDTLHQVHLLCAWLEILMGLVWRSMHPGKLLFAPNLLLDNRQCKVEGVVEI 120  
 DB 369 PGFGLDLHQVHLLCAWLEILMGLVWRSMHPGKLLFAPNLLLDNRQCKVEGVVEI 428  
 QY 121 FDMLLATSSFRMNLQGEFVCLKSIILLNSGYVTFPXXXXXXSEKDHHRVLDKIT 180  
 DB 429 FDMLLATSSFRMNLQGEFVCLKSIILLNSGYVTF-LGSLTKSLEEKDHHRVLDKIT 487  
 QY 181 DTLLHMAKAGLTQQOQHRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPVLDLLEM 240  
 DB 488 DTLLHMAKAGLTQQOQHRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPVLDLLEM 547  
 QY 241 LDAHRL 246  
 DB 548 LDAHRL 553  
 RESULT 5  
 ESRI\_RAT  
 ID ESRI\_RAT STANDARD; PRT; 600 AA.  
 AC P06211;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).  
 GN Name=Esrl; Synonyms=Nr3a1, Esr, Esr1;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar;  
 RA Muramatsu M.;  
 RL Submitted (MAR-1987) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87174780; PubMed=3031601;  
 RA Koike S., Sakai M.;  
 RT "Molecular cloning and characterization of rat estrogen receptor  
 cDNA".  
 RL Nucleic Acids Res. 15:2499-2513(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Uterus;  
 RA Maggi A.M.A.;  
 RL Submitted (JUN-1991) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP INTERACTION WITH UBE1C.  
 RX PubMed=11818503;  
 RA Fan M., Long X., Bailey J.A., Reed C.A., Osborne E., Gize E.A.,  
 RA Kirk E.A., Bigsby R.M., Nephew K.P.;  
 RT "The activating enzyme of NEDD8 inhibits steroid receptor function.";  
 RL Mol. Endocrinol. 16:315-330(2002).  
 CC -!- FUNCTION: Nuclear hormone receptor. The steroid hormones and their  
 CC receptors are involved in the regulation of eukaryotic gene  
 CC expression and affect cellular proliferation and differentiation  
 CC in target tissues.  
 CC -!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with  
 CC ESR2. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading  
 CC to a strong increase of transcription of target genes (By  
 CC similarity). Binds UBE1C.  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,  
 CC a DNA-binding domain and a C-terminal steroid-binding domain.  
 CC -!- PM: Phosphorylated by cyclin A/CDK2 (By similarity).  
 CC -!- MISCELLANEOUS: In the absence of ligand, steroid hormone receptors  
 CC are thought to be weakly associated with nuclear components;  
 CC hormone binding greatly increases receptor affinity. The hormone-  
 CC receptor complex appears to recognize discrete DNA sequences  
 CC upstream of transcriptional start sites.  
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3  
 CC subfamily.  
 -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/ebis/announcements>)  
 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk).  
 -----  
 CC EMBL; Y00102; CAA68287.1; -;  
 DR EMBL; X61098; CAA43411.1; -;  
 DR PIR; S07379; QRTE.  
 DR HSP; P03372; IHCP.  
 DR TRANSFAC; T00258; -;  
 DR RGD; 2581; Esrl.  
 DR GO; GO:0016049; P:cell growth; ISS.  
 DR GO; GO:0045839; P:negative regulation of mitosis; ISS.  
 DR InterPro; IPR000536; Hrmn\_recept\_lig.  
 DR InterPro; IPR001292; Oestrgn\_receptor.  
 DR InterPro; IPR001723; Strhmrn\_receptor.  
 DR InterPro; IPR008946; Str\_ncl\_receptor.  
 DR InterPro; IPR001628; Znf\_C4steroid.  
 DR Pfam; PF00104; Hormone\_recep; 1.  
 DR Pfam; PF02159; Oest\_recep; 1.  
 DR Pfam; PF00105; zf-C4; 1.  
 DR PRINTS; PR00543; OESTROGENR.  
 DR PRINTS; PR00398; STRDHORMONER.  
 DR PRINTS; PR00047; STROIDFINGER.  
 DR PRODOM; PD000035; Znf\_C4steroid; 1.  
 DR SMART; SM00430; HOLI; 1.  
 DR SMART; SM00399; Znf\_C4; 1.

```
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Phosphorylation; Receptor;
KW Steroid-binding; Transcription regulation; Zinc-finger.
FT DOMAIN 1 189 Modulating.
FT DNA_BIND 190 255 Nuclear receptor-type.
FT ZN_FING 190 210 C4-type.
FT ZN_FING 226 250 C4-type.
FT DOMAIN 256 315 Hinge.
FT DOMAIN 316 600 Steroid-binding.
FT DOMAIN 64 71 Poly-Ala.
FT DOMAIN 171 174 Poly-Ser.
FT MOD_RES 109 109 Phosphoserine (by CDK2) (By similarity).
FT MOD_RES 111 111 Phosphoserine (by CDK2) (By similarity).
FT MOD_RES 123 123 Phosphoserine (By similarity).
FT MOD_RES 172 172 Phosphoserine (by CK2) (By similarity).
FT MOD_RES 542 542 Phosphotyrosine (by Tyr-Kinases) (By similarity).
FT CONFLICT 488 488 N -> T (in Ref. 3).
SQ SEQUENCE 600 AA; 67030 MW; C9C7D8CACB0F57D8 CRC64;

Query Match 94.7%; Score 1167.5; DB 1; Length 600;
Best Local Similarity 92.7%; Pred. No. 1.2e-105;
Matches 228; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 SLALSLTADQMSVALLDAEPPIYSEYDPTFRPFSEASMMGLLTNLADRELVHMINWAKRV 60
DB 310 SPALSLTADQMSVALLDAEPPIYSEYDPTFRPFSEASMMGLLTNLADRELVHMINWAKRV 369
QY 61 PGFVDLTLDQVHLLCAWLEIMTGLVWRSMHFGKLLFAPNLLDRNQKCVGMEI 120
DB 370 PGFGDLNLHDQVHLLCAWLEIMTGLVWRSMHFGKLLFAPNLLDRNQKCVGMEI 429
QY 121 FDMLLATSSRFMRNNLQGEFEVCLSKIIILNLSGVYTFXXXXXXEKKDHRVLDKIT 180
DB 430 FDMLLATSSRFMRNNLQGEFEVCLSKIIILNLSGVYTF-LSSSTLKSLEEKDHRVLDKIT 488
QY 181 DTLIHLMAKAGTLQOQHRLAQLLLSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLHM 240
DB 489 DTLIHLMAKAGTLQOQHRLAQLLLSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLHM 548
QY 241 LDAHRL 246
DB 549 LDAHRL 554

RESULT 6
ESR1_PIG STANDARD; PRT; 595 AA.
AC 9040;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
GN Names=ESR1; Synonyms=NR3A1, ESR;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RS SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Uterus;
RA MEDLINE=95080454; PubMed=7988744;
RA Boekenkamp D., Jungblut P.W., Thole H.H.;
RT "The C-terminal half of the porcine estradiol receptor contains no
RT post-translational modification: determination of the primary
RT structure."
RL Mol. Cell. Endocrinol. 104:163-172(1994).
CC -!- FUNCTION: Nuclear hormone receptor. The steroid hormones and their
CC receptors are involved in the regulation of eukaryotic gene
CC expression and affect cellular proliferation and differentiation
CC in target tissues (By similarity).
CC -!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with
CC ESR2. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading
```

Qy 61 PGFVDTLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 120  
 Db 365 PGFLDLSLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 424  
 Qy 121 FDMLLATSSRRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXBEKDHHRVLDKIT 180  
 Db 425 FDMLLATSSRRMNLQGEFVCLKSIILLNSGVYTF-LSSLTKSLEKDHHRVLDKIT 483  
 Qy 181 DTLHLMKAGLTQQOHRQAQLLLILSHIRMSNKGMEHLYSMKCNVVPVYDLLLLL 240  
 Db 484 DTLHLMKAGLTQQOHRQAQLLLILSHIRMSNKGMEHLYSMKCNVVPVYDLLLLL 543  
 Qy 241 LDAHRL 246  
 Db 544 LDAHRL 549

RESULT 7  
 ES QSAU  
 ID QSAU STANDARD; PRT; 595 AA.  
 AC Q9QZJ5; Q9QZG6;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).  
 GN Name=ESR1; Synonyms=NR3A1, ESR;  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RX MEDLINE=20197937; PubMed=10731637;  
 RA Bhat H.K., Vadgama J.V.;  
 RT "Hamster estrogen receptor cDNA: cloning and mRNA expression.";  
 RL J. Steroid Biochem. Mol. Biol. 72:47-53(2000).  
 RN [2]  
 RP SEQUENCE OF 98-291 FROM N.A.  
 RA Jones J.E., Carpenter C.D., Lubbers L.S., Petersen S.L., Wade G.N.;  
 RT "Return of lordosis after food deprivation and refeeding in Syrian hamsters.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Nuclear hormone receptor. The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues (By similarity).  
 CC -1- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with ESR2. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading to a strong increase of transcription of target genes. Binds UBE1C (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.  
 CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3 subfamily.

-----  
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 EMBL; AF181077; AAD53956.1; -;  
 EMBL; AF184276; AAF02721.1; -;  
 HSSP; P03372; IHCQ.  
 GO; GO:0016585; C:chromatin remodeling complex; ISS.  
 GO; GO:0016020; C:membrane; ISS.  
 GO; GO:0030284; F:estrogen receptor activity; ISS.

GO; GO:0030235; F:nitric-oxide synthase regulator activity; ISS.  
 GO; GO:0016049; P:cell growth; ISS.  
 GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.  
 GO; GO:0045839; P:negative regulation of mitosis; ISS.  
 GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.  
 InterPro; IPR000536; Hrmn\_recept\_lig.  
 InterPro; IPR001292; Oestrgn\_receptor.  
 InterPro; IPR001723; Strdhrmn\_receptor.  
 InterPro; IPR008946; Str\_ncl\_receptor.  
 InterPro; IPR001628; Znf\_C4steroid.  
 Pfam; PF001104; Hormone\_recep; 1.  
 Pfam; PF021159; Oest\_recep; 1.  
 Pfam; PF021105; zf-C4; 1.  
 PRINTS; PR00543; OESTROGENR.  
 PRINTS; PR00398; STRDHORMONER.  
 PRINTS; PR00047; STROIDFINGER.  
 ProDom; PD000035; Znf\_C4steroid; 1.  
 SMART; SM00430; HOL1; 1.  
 SMART; SM00399; Znf\_C4; 1.  
 PROSITE; PS00031; NUCLEAR RECEPTOR; 1.  
 DNA-binding; Nuclear protein; Phosphorylation; Receptor;  
 Steroid-binding; Transcription regulation; Zinc-finger.  
 DOMAIN 1 184  
 DNA\_BIND 185 250  
 ZN\_FING 185 205  
 ZN\_FING 221 245  
 DOMAIN 251 310  
 HINGE  
 DOMAIN 311 551  
 Steroid-binding.  
 DOMAIN 112 115  
 Poly-Pro.  
 DOMAIN 166 169  
 Poly-Ser.  
 MOD\_RES 103 103  
 Phosphoserine (by CDK2) (By similarity).  
 MOD\_RES 105 105  
 Phosphoserine (by CDK2) (By similarity).  
 MOD\_RES 118 118  
 Phosphoserine (By similarity).  
 MOD\_RES 167 167  
 Phosphoserine (by CK2) (By similarity).  
 MOD\_RES 537 537  
 Phosphotyrosine (by Tyr-kinase) (By similarity).  
 CONFLICT 98 99  
 QL -> PF (in Ref. 2).  
 FT CONFLICT 144 144  
 S -> T (in Ref. 2).  
 FT CONFLICT 198 199  
 GV -> EVEQI (in Ref. 2).  
 FT CONFLICT 290 291  
 NL -> KG (in Ref. 2).  
 SQ SEQUENCE 595 AA; 66833 MW; E4D803B4FFDB257E CRC64;

Query Match 94.3%; Score 1159.5; DB 1; Length 595;  
 Best Local Similarity 91.5%; Pred. No. 7.3e-105;  
 Matches 225; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

Qy 1 SLALSITADQVMSALLDAEPPIYSEYDPRPSEASMMGLLTNLADRELVHMINKRV 60  
 Db 305 SPALSITADQVMSALLDAEPPIYSEYDPRPSEASMMGLLTNLADRELVHMINKRV 364  
 Qy 61 PGFVDTLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 120  
 Db 365 PGFVDTLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 424  
 Qy 121 FDMLLATSSRRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXBEKDHHRVLDKIT 180  
 Db 425 FDMLLATSSRRMNLQGEFVCLKSIILLNSGVYTF-LSSLTKSLEKDHHRVLDKIT 483  
 Qy 181 DTLHLMKAGLTQQOHRQAQLLLILSHIRMSNKGMEHLYSMKCNVVPVYDLLLLL 240  
 Db 484 DTLHLMKAGLTQQOHRQAQLLLILSHIRMSNKGMEHLYSMKCNVVPVYDLLLLL 543  
 Qy 241 LDAHRL 246  
 Db 544 LDAHRL 549

RESULT 8  
 Q8UW50  
 ID Q8UW50 PRELIMINARY; PRT; 587 AA.  
 AC Q8UW50;  
 DT 01-MAR-2002 (T:EMBLrel. 20, Created)  
 DT 01-MAR-2002 (T:EMBLrel. 20, Last sequence update)

```
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Estrogen receptor.
OS Caiman crocodilus (Spectacled caiman) (Caiman sclerops).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Caiman.
OX NCBI_TaxID=8499;
RN [1]_TaxID=8499;
RP SEQUENCE FROM N.A.
RX MEDLINE=21490797; PubMed=11604222;
RA Sumida K., Ooe N., Saito K., Kaneko H.;
RT "Molecular cloning and characterization of reptilian estrogen receptor
  cDNA".
RL Mol. Cell. Endocrinol. 183:33-39(2001).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
DE EMBL; AB055220; BAB79436.1; -.
DR HSSP; P03372; 1HCP.
DR GO; GO:0016585; C:chromatin remodeling complex; ISS.
DR GO; GO:0016020; C:membrane; ISS.
DR GO; GO:0030284; F:estrogen receptor activity; ISS.
DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; ISS.
DR GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
DR InterPro; IPR000536; Hmon_recept_lig.
DR InterPro; IPR001292; Oestrgn_receptor.
DR InterPro; IPR001723; Strhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF02159; Oest_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00543; OESTROGENR.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI_1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00311; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 587 AA; 66513 MW; DE17F2B837FCF513 CRC64;

Query Match          93.2%; Score 1146.5; DB 2; Length 587;
Best Local Similarity 90.7%; Pred.No. 1.3e-103;
Matches 223; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 1 SLALSITADQVMSALDABPPILYSEYDTPFPSEASMMGLLTNLADRELVHMINWAKRV 60
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 299 SPALSITAEQVMSALLAEAPPIVYSEYDNPFPNEASMTLLTNLADRELVHMINWAKRV 358
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVRSMEHPGKLLFAPNLLLDNRQKCVGEMVEI 120
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 359 PGFVDLTLDQVHLLCAWLEILMIGLVRSMEHPGKLLFAPNLLLDNRQKCVGEMVEI 418
QY 121 FQMLLATSSRFRRMNLQGFEEVCKLSIILNLSGVYTFXXXXXXEEDKHRLVLDKIT 180
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 419 FQMLLATSAFRFRMNLQGFEEVCKLSIILNLSGVYTF-LSSLTLSLEEDKHRLVLDKIT 477
QY 181 DTILHLMKAGLTLOQOORLAQLLILSHIRMSNKGHEHLYSMCKKNVPLYDILLLEM 240
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 478 DTILHLMKAGLTLOQOORLAQLLILSHIRMSNKGHEHLYSMCKKNVPLYDILLLEM 537
QY 241 LDAHRL 246
DQ |||||
Db 538 LDAHRL 543

RESULT 9
ESR1_HORSE STANDARD; PRT; 594 AA.
AC Q9TV98;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
GN Name=ESR1; Synonyms=NR3A1, ESR;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]_TaxID=9796;
RP SEQUENCE FROM N.A.
RX McDowell K.J., Adams M.H., Green M.L., Cleaver B.D., Sharp D.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Nuclear hormone receptor. The steroid hormones and their
  receptors are involved in the regulation of eukaryotic gene
  expression and affect cellular proliferation and differentiation
  in target tissues (By similarity). Can form a heterodimer with
  ESR2. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading
  to a strong increase of transcription of target genes.Binds UBE1C
  (By similarity).
CC -!- SUBUNIT: Binds DNA as a homodimer.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
  a DNA-binding domain and a C-terminal steroid-binding domain.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
  subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF124093; AAD17316.1; -.
DR HSSP; P03372; 1HCP.
DR GO; GO:0016585; C:chromatin remodeling complex; ISS.
DR GO; GO:0016020; C:membrane; ISS.
DR GO; GO:0030284; F:estrogen receptor activity; ISS.
DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; ISS.
DR GO; GO:0016049; P:cell growth; ISS.
DR GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.
DR GO; GO:0045839; P:negative regulation of mitosis; ISS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
DR InterPro; IPR000536; Hmon_recept_lig.
DR InterPro; IPR001292; Oestrgn_receptor.
DR InterPro; IPR001723; Strhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF02159; Oest_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00543; OESTROGENR.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI_1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00311; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Phosphorylation; Receptor;
KW Steroid-binding; Transcription regulation; Zinc-finger.
FT DOMAIN 1 184 Modulating.
FT DNA_BIND 185 250 Nuclear receptor-type.
FT ZN_FING 185 205 C4-type.
FT ZN_FING 221 245 C4-type.
FT DOMAIN 251 310 Hinge.
FT DOMAIN 311 550 Steroid-binding.
FT DOMAIN 64 70 Poly-Ala.
FT MOD_RES 104 104 Phosphoserine (by CDK2) (By similarity).
FT MOD_RES 106 106 Phosphoserine (by CDK2) (By similarity).
FT MOD_RES 118 118 Phosphoserine (By similarity).
FT MOD_RES 167 167 Phosphoserine (by CK2) (By similarity).
FT MOD_RES 536 536 Phosphotyrosine (by Tyr-kinases) (By
  similarity).
```

SQ SEQUENCE 594 AA; 66103 MW; DD36CA7C24C74B95 CRC64;

Query Match 93.2%; Score 1146; DB 1; Length 594;  
 Best Local Similarity 91.5%; Pred. No. 1.5e-103;  
 Matches 225; Conservative 7; Mismatches 12; Indels 2; Gaps 2;

QY 1 SLALSLTADQWVSALLDAEPPIYSEYDPTPTFSEASMMGLLTNLADRELVHMINAKRV 60  
 DB 305 SPVLSLTAEQVMSALLDAEPPIYSEYDPTPTFSEASMMGLLTNLADRELVHMINAKRV 364  
 QY 61 PGFVDLTLDHVDHLLCAWLEILMGLVWRSMEHPGKLLFAPNLLLDNRQKCVGVEI 120  
 DB 365 PGFVDLSLDHVDHLLCAWLEILMGLVWRSMEHPGKLLFAPNLLLDNRQKCVGVEI 424  
 QY 121 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEKDHHRVLDKIT 180  
 DB 425 FDMLLATSSRLRMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEKDHHRVLDKIT 483  
 QY 181 DTLLHLMKAGLTLOQOHRLAQLLLILSHIRHNSKMGHEHLYSMKCNVVPVLDLLEM 240  
 DB 484 DTLLHLMKAGLTLOQOHRLAQLLLILSHIRHNSKMGHEHLYSMKCNVVPVLDLLEM 542  
 QY 241 LDAHRL 246  
 DB 543 LDAHRL 548

RESULT 10  
 ESRL\_POEQU STANDARD; PRT; 587 AA.  
 ID ESRL\_POEQU STANDARD; PRT; 587 AA.  
 AC Q91250;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).  
 GN Name=ESR1; Synonyms=NR3A1; ESR; (Taeniopygia guttata).  
 OS Poephila guttata (Zebra finch) (Taeniopygia guttata).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;  
 OC Estrilidae; Taeniopygia.  
 OX NCBI\_TaxID=59729;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Hypothalamus;  
 RA Jacobs E.C.; Arnold A.P.; Campagnoni A.T.;  
 RT "Zebra finch estrogen receptor cDNA: cloning and mRNA expression.";  
 RL Steroid Biochem. Mol. Biol. 59:135-145(1996).  
 CC - FUNCTION: The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues.  
 CC - SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with ER-beta (By similarity).  
 CC - SUBCELLULAR LOCATION: Nuclear.  
 CC - DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.  
 CC - SIMILARITY: Belongs to the nuclear hormone receptor family. NR3 subfamily.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; L79911; AAB81108.1; -;  
 CC HSSP; P03372; IHP.  
 DR GO: GO:0016585; C:chromatin remodeling complex; ISS.  
 DR GO: GO:0016020; C:membrane; ISS.  
 DR GO: GO:0030284; F:estrogen receptor activity; ISS.  
 DR GO: GO:0030235; F:nitric-oxide synthase regulator activity; ISS.

DR GO: GO:0030520; P:estrogen receptor signaling pathway; ISS.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; ISS.  
 DR InterPro: IPR000536; H:monomer receptor.  
 DR InterPro: IPR001292; O:estrogen receptor.  
 DR InterPro: IPR001723; S:cdhmn\_receptor.  
 DR InterPro: IPR008946; S:cdhmn\_receptor.  
 DR InterPro: IPR001628; Znf\_C4steroid.  
 DR Pfam: PF00104; Hormone recep; 1.  
 DR Pfam: PF02159; Oest recep; 1.  
 DR Pfam: PF00105; zf-C4; 1.  
 DR PRINTS; PR00543; OESTROGENR.  
 DR PRINTS; PR00398; STRDHORMONER.  
 DR PRINTS; PR00047; STROIDFINGER.  
 DR ProDom: PD000035; Znf\_C4steroid; 1.  
 DR SMART; SM00430; HOL1; 1.  
 DR SMART; SM00399; Znf\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
 KW DNA-binding; Nuclear protein; Receptor; Steroid-binding;  
 KW Transcription regulation; Zinc-finger.  
 FT DOMAIN 1 176 Modulating.  
 FT DNA BIND 177 242 Nuclear receptor-type.  
 FT ZN\_FING 177 197 C4-type.  
 FT ZN\_FING 213 237 C4-type.  
 FT DOMAIN 243 302 Hinge.  
 FT DOMAIN 303 587 Steroid-binding.  
 SQ SEQUENCE 587 AA; 66553 MW; 2B254168A7A910AB CRC64;

Query Match 93.0%; Score 1144.5; DB 1; Length 587;  
 Best Local Similarity 90.2%; Pred. No. 2.1e-103;  
 Matches 222; Conservative 12; Mismatches 11; Indels 1; Gaps 1;

QY 1 SLALSLTADQWVSALLDAEPPIYSEYDPTPTFSEASMMGLLTNLADRELVHMINAKRV 60  
 DB 297 SPALSLTAEQVMSALLDAEPPIYSEYDPTPTFSEASMMGLLTNLADRELVHMINAKRV 356  
 QY 61 PGFVDLTLDHVDHLLCAWLEILMGLVWRSMEHPGKLLFAPNLLLDNRQKCVGVEI 120  
 DB 357 PGFVDLTLDHVDHLLCAWLEILMGLVWRSMEHPGKLLFAPNLLLDNRQKCVGVEI 416  
 QY 121 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEKDHHRVLDKIT 180  
 DB 417 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEKDHHRVLDKIT 475  
 QY 181 DTLLHLMKAGLTLOQOHRLAQLLLILSHIRHNSKMGHEHLYSMKCNVVPVLDLLEM 240  
 DB 476 DTLLHLMKAGLTLOQOHRLAQLLLILSHIRHNSKMGHEHLYSMKCNVVPVLDLLEM 535  
 QY 241 LDAHRL 246  
 DB 536 LDAHRL 541

RESULT 11  
 ESRL\_CHICK STANDARD; PRT; 589 AA.  
 ID ESRL\_CHICK STANDARD; PRT; 589 AA.  
 AC P06212;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).  
 GN Name=ESR1; Synonyms=NR3A1; ESR;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86247578; PubMed=3755102;  
 RA Krust A.; Green S.; Argos P.; Kumar V.; Walter P.; Bornert J.-M.;  
 RA Chambon P.;  
 RT "The chicken estrogen receptor sequence: homology with v-erbA and the human estrogen and glucocorticoid receptors.";

RL EMBO J. 5:891-897(1986).  
 CC -!- FUNCTION: The steroid hormones and their receptors are involved in  
 CC the regulation of eukaryotic gene expression and affect cellular  
 CC proliferation and differentiation in target tissues.  
 CC -!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with ER-  
 CC beta.  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,  
 CC a DNA-binding domain and a C-terminal steroid-binding domain.  
 CC -!- MISCELLANEOUS: In the absence of ligand, steroid hormone receptors  
 CC are thought to be weakly associated with nuclear components;  
 CC hormone binding greatly increases receptor affinity. The hormone-  
 CC receptor complex appears to recognize discrete DNA sequences  
 CC upstream of transcriptional start sites.  
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3  
 CC subfamily.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
 CC -----  
 DR EMBL; X03805; CAA27433.1; -.  
 DR FIR; A40914; QRCHE.  
 DR HSSP; P03372; IHCP.  
 DR TRANSFAC; T00264; -.  
 DR GO; GO:0016585; C:chromatin remodeling complex; ISS.  
 DR GO; GO:0016020; C:membrane; ISS.  
 DR GO; GO:0030284; F:estrogen receptor activity; ISS.  
 DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; ISS.  
 DR GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.  
 DR InterPro; IPR000536; P:regulation of transcription, DNA-dependent; ISS.  
 DR InterPro; IPR001292; Oestrgn\_receptor.  
 DR InterPro; IPR001723; Strdhmn\_receptor.  
 DR InterPro; IPR008946; Str\_ncl\_receptor.  
 DR InterPro; IPR001628; Znf\_C4steroid.  
 DR Pfam; PF00104; Hormone\_recep; 1.  
 DR Pfam; PF02159; Oest\_recep; 1.  
 DR Pfam; PF00105; zf-C4; 1.  
 DR PRINTS; PR00543; OESTROGENR.  
 DR PRINTS; PR00398; STRDHORMONER.  
 DR PRINTS; PR00047; STROIDFINGER.  
 DR ProDom; PD000035; Znf\_C4steroid; 1.  
 DR SMART; SM00430; HOLI; 1.  
 DR SMART; SM00399; ZNF\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
 DR DNA-binding; Nuclear protein; Receptor; Steroid-binding;  
 KW Transcription regulation; Zinc-finger.  
 FT DOMAIN 1 178 Modulating.  
 FT DNA\_BIND 179 244 Nuclear receptor-type.  
 FT ZN\_FING 179 199 C4-type.  
 FT ZN\_FING 215 239 C4-type.  
 FT DOMAIN 245 304 Hinge.  
 FT DOMAIN 305 589 Steroid-binding.  
 SQ SEQUENCE 589 AA; 66746 MW; 1B092233C770A54B CRC64;  
 Query Match 93.0%; Score 1143.5; DB 1; Length 589;  
 Best Local Similarity 90.2%; Pred. No. 2.7e-103;  
 Matches 222; Conservative 12; Mismatches 11; Indels 1; Gaps 1;  
 QY 1 SLALSLTADQWVSALLDAPPPILYSEYDPTFPFSEASMMGLLTNLADRELVHMINWAKRV 60  
 DB 299 SPALSLTAQWVSALLAEAPPVIVSEYDPTFPFNEASMMWTLTNLADRELVHMINWAKRV 358  
 QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGWEI 120  
 DB 359 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGWEI 418  
 QY 121 FQMLLATSSRRFRMNNLQGEFEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRLVDKIT 180  
 DB 419 FQMLLATSSRRFRMNNLQGEFEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRLVDKIT 477

Db 419 FQMLLATSSRRFRMNNLQGEFEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRLVDKIT 477  
 QY 181 DTLIHLMAKAGLTITQQQHQAQLLLILSHIRHMSKGMHEHLYSMKCKNVVPLYLLEEM 240  
 Db 478 DTLIHLMAKAGLTITQQQHQAQLLLILSHIRHMSKGMHEHLYSMKCKNVVPLYLLEEM 537  
 QY 241 LDAHRL 246  
 Db 538 LDAHRL 543  
 RESULT 12  
 Q765N7 PRELIMINARY; PRT; 587 AA.  
 AC Q765N7;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Estrogen receptor a.  
 GN Name=Era;  
 OS Alligator mississippiensis (American alligator).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.  
 OX NCBI\_TaxID=8496;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Gonad;  
 RX PubMed=14980803;  
 RA Katsu Y., Bermudez D.S., Braun E.L., Helbing C., Miyagawa S.,  
 RA Gunderson M.P., Kohno S., Bryan T.A., Guillelte L.J., Iguchi T.;  
 RT "Molecular cloning of the estrogen and progesterone receptors of the  
 RT American alligator.";  
 RL Gen. Comp. Endocrinol. 136:122-133 (2004).  
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.  
 DR EMBL; AB115909; BAD08348.1; -.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR000536; Hmonn\_recept\_lig.  
 DR InterPro; IPR001292; Oestrgn\_receptor.  
 DR InterPro; IPR001723; Strdhmn\_receptor.  
 DR InterPro; IPR008946; Str\_ncl\_receptor.  
 DR InterPro; IPR001628; Znf\_C4steroid.  
 DR Pfam; PF00104; Hormone\_recep; 1.  
 DR Pfam; PF02159; Oest\_recep; 1.  
 DR Pfam; PF00105; zf-C4; 1.  
 DR PRINTS; PR00543; OESTROGENR.  
 DR PRINTS; PR00398; STRDHORMONER.  
 DR PRINTS; PR00047; STROIDFINGER.  
 DR ProDom; PD000035; Znf\_C4steroid; 1.  
 DR SMART; SM00430; HOLI; 1.  
 DR SMART; SM00399; ZNF\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
 KW DNA-binding; Metal-binding; Nuclear protein; Receptor;  
 KW Transcription regulation; Zinc; Zinc-finger.  
 SQ SEQUENCE 587 AA; 66497 MW; FC217FCC0F1B41F0 CRC64;  
 Query Match 92.9%; Score 1142.5; DB 2; Length 587;  
 Best Local Similarity 90.2%; Pred. No. 3.3e-103;  
 Matches 222; Conservative 12; Mismatches 11; Indels 1; Gaps 1;

QY 1 SLALSLTADQWVSALLDAPPPILYSEYDPTFPFSEASMMGLLTNLADRELVHMINWAKRV 60  
 DB 299 SPALSLTAQWVSALLAEAPPVIVSEYDPTFPFNEASMMWTLTNLADRELVHMINWAKRV 358  
 QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGWEI 120  
 DB 359 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGWEI 418  
 QY 121 FQMLLATSSRRFRMNNLQGEFEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRLVDKIT 180  
 DB 419 FQMLLATSSRRFRMNNLQGEFEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRLVDKIT 477

QY 181 DTLIHLMAKAGLTQQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEM 240  
Db 478 DTLIHLMAKAGLTQQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEM 537  
QY 241 LDAHRL 246  
Db 538 LDAHRL 543

## RESULT 13

BAD08348 PRELIMINARY; PRT; 587 AA.  
AC BAD08348;  
DT 14-APR-2004 (TReMBLrel. 27, Created)  
DT 14-APR-2004 (TReMBLrel. 27, Last sequence update)  
DT 14-APR-2004 (TReMBLrel. 27, Last annotation update)  
DE Estrogen receptor a.  
GN ERA  
OS Alligator mississippiensis (American alligator).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.  
OX NCBI\_TaxID=8496;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Gonad;  
RA Katsu Y., Bermudez D.S., Braun E.L., Helbing C., Miyagawa S.,  
RA Gunderson M.P., Kohno S., Bryan T.A., Guillet L.J., Iguchi T.;  
RT "Molecular cloning of the estrogen and progesterone receptors of the  
RT American alligator";  
RL Gen. Comp. Endocrinol. 136:122-133 (2004).  
KW EMBL; AB115909; BAD08348.1; -.  
KW Receptor.

QY SEQUENCE 587 AA; 66497 MW; FC217PCCOF1B41F0 CRC64;

Query Match 92.9%; Score 1142.5; DB 2; Length 587;

Best Local Similarity 90.2%; Pred. No. 3.3e-103; Indels 1; Gaps 1;  
Matches 222; Conservative 12; Mismatches 11;

QY 1 SLALSITADQVMSALLDAEPPIVSEYDPTPPFSEASMMGLLTNLADRELVHMINAKRV 60  
Db 299 SPALSLTAEQVMSALLAEPIVSEYDPTPPFSEASMMGLLTNLADRELVHMINAKRV 358  
QY 61 PGFVDLTLDQVHLLCAWLEILMGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEVEI 120  
Db 359 PGFVDLTLDQVHLLCAWLEILMGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEVEI 418  
QY 121 FDMLLATSSFRMNLQGEFVCLKSIILLNSGYTTFXXXXXXSEKHHRVLDKIT 180  
Db 419 FDMLLATAARFRMNLQGEFVCLKSIILLNSGYTTF-LSSTLKSLEEKDYIHRVLDKIT 477  
QY 181 DTLIHLMAKAGLTQQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEM 240  
Db 478 DTLIHLMAKAGLTQQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEM 537  
QY 241 LDAHRL 246  
Db 538 LDAHRL 543

## RESULT 14

Q8AYHO PRELIMINARY; PRT; 589 AA.  
AC Q8AYHO;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Estrogen receptor alpha.  
OS Coturnix coturnix japonica (Japanese quail).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Coturnix.  
OX NCBI\_TaxID=93934;  
RN [1]

## SEQUENCE FROM N.A.

RP TISSUE=Liver;  
RA Ichikawa K., Yamamoto I., Tsukada A., Saito N., Shimada K.;  
RA Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
RL -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family.  
CC EMBL; AF442965; AAN63674.1; -.  
DR HSSP; P03372; 1HCP.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0005496; F:steroid binding; IEA.  
DR GO; GO:0003707; F:steroid hormone receptor activity; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR000536; Hrmn recept lig.  
DR InterPro; IPR01292; Oestrgn receptor.  
DR InterPro; IPR001723; Strdhmn\_receptor.  
DR InterPro; IPR008946; Str\_ncl\_receptor.  
DR InterPro; IPR001628; Znf\_C4steroid.  
DR Pfam; PF00104; Hormone recep; 1.  
DR Pfam; PF02159; Oest recep; 1.  
DR Pfam; PF00105; zf-C4; 1.  
DR PRINTS; PR00543; OESTROGENR.  
DR PRINTS; PR00398; STRDHMONER.  
DR PRINTS; PR00047; STROIDFINGER.  
DR PRODom; PD000035; Znf\_C4steroid; 1.  
DR SMART; SM00430; HOL1; 1.  
DR SMART; SM00399; ZNF C4; 1.  
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.  
KW DNA-binding; Metal-binding; Nuclear protein; Receptor;  
KW Transcription regulation; Zinc; Zinc-finger.  
SQ SEQUENCE 589 AA; 66767 MW; 8271FDAA67552CA4 CRC64;

Query Match 92.6%; Score 1139.5; DB 2; Length 589;

Best Local Similarity 89.8%; Pred. No. 6.6e-103; Indels 1; Gaps 1;  
Matches 221; Conservative 12; Mismatches 12;

QY 1 SLALSITADQVMSALLDAEPPIVSEYDPTPPFSEASMMGLLTNLADRELVHMINAKRV 60  
Db 299 SPALSLTAEQVMSALLAEPIVSEYDPTPPFSEASMMGLLTNLADRELVHMINAKRV 358  
QY 61 PGFVDLTLDQVHLLCAWLEILMGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEVEI 120  
Db 359 PGFVDLTLDQVHLLCAWLEILMGLVWRSMEHPGKLLFAPNLLDRNQKCVGMEVEI 418  
QY 121 FDMLLATSSFRMNLQGEFVCLKSIILLNSGYTTFXXXXXXSEKHHRVLDKIT 180  
Db 419 FDMLLATAARFRMNLQGEFVCLKSIILLNSGYTTF-LSSTLKSLEERDIHRVLDKIT 477  
QY 181 DTLIHLMAKAGLTQQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEM 240  
Db 478 DTLIHLMAKAGLTQQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEM 537  
QY 241 LDAHRL 246  
Db 538 LDAHRL 543

## RESULT 15

Q8CGK8 PRELIMINARY; PRT; 353 AA.  
AC Q8CGK8;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Estrogen receptor alpha (Fragment).  
GN Name=ESR1;  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Uterus;

RA Zhang X., Harris H.;  
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
CC -|- SUBCELLULAR LOCATION: Nuclear (By similarity).  
CC -|- SIMILARITY: Belongs to the nuclear hormone receptor family.  
DR EMBL; AY172106; AAN85120.1; -.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003707; F:steroid hormone receptor activity; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR000536; Hrmn\_recept\_lig.  
DR InterPro; IPR001723; Stdhrmn\_receptor.  
DR InterPro; IPR008946; Str\_ncl\_receptor.  
DR InterPro; IPR001628; Znf\_C4steroid.  
DR Pfam; PF00104; Hormone\_recep; 1.  
DR Pfam; PF00105; zf-C4; 1.  
DR PRINTS; PR00398; STRDHORMONER.  
DR SMART; SM00430; HOL1; 1.  
KW DNA-binding; Metal-binding; Nuclear protein; Receptor;  
KW Transcription regulation; Zinc; Zinc-finger.  
FT NON\_TER 1  
SQ SEQUENCE 353 AA; 40099 MW; C298827350700510 CRC64;  
  
Query Match 92.5%; Score 1137.5; DB 2; Length 353;  
Best Local Similarity 89.4%; Pred. NO. 5.7e-103;  
Matches 220; Conservative 12; Mismatches 13; Indels 1; Gaps 1;  
  
QY 1 SLALSITADQMSALDAPPTLYSEYDTPRPSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 63 SPALSITADQMSALDAPPTLYSEYDAVKPPSEASMMGLLTNLADRELVHMINWAKRV 122  
  
QY 61 PGFVDLTLDQVHLLCAWLEIMGLVWRSMEHPGKLLPAPNLLIDRNQKCGVEGMVEI 120  
DB 123 PGFGDLTLDQVHLLCAWLEIMGLIWRSEHPGKLLPAPNLLIDRNQKCGVEGMVEI 182  
  
QY 121 FDMLLATSRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXEEXKHHRVLDKIT 180  
DB 183 FDMLLATSRFRMNLQGEFVCLKSIILLNSGVYTF-LSSSTLKSLEEXKHHRVLDKIT 241  
  
QY 181 DTLIHLMKAGLTLOOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKVVPVLYDLLEEM 240  
DB 242 DTLIHLMKAGLTLOOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKVVPVLYDLLEEM 301  
  
QY 241 LDAHRL 246  
DB 302 LEAHL 307

Search completed: November 8, 2004, 08:28:00  
Job time : 46.1837 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2004, 08:14:27 ; Search time 12.049 Seconds  
(without alignments)  
1964.426 Million cell updates/sec

Title: US-09-830-693B-28  
Perfect score: 1230  
Sequence: 1 SLAULTADQMSALLDAEP.....CKNVVPLYDLLEMLDAHRL 246  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1197.5	97.4	595	1 QRHUE	estrogen receptor
2	1171.5	95.2	599	1 QRMSE	estrogen receptor
3	1167.5	94.9	600	1 QRTTE	estrogen receptor
4	1164.5	94.7	595	2 I47140	estradiol receptor
5	1145.5	93.1	701	2 S64737	80K estrogen recep
6	1143.5	93.0	589	1 QRCXE	estrogen receptor
7	1037.5	84.3	586	1 QRXLE	estrogen receptor
8	792.5	64.4	620	2 T10423	estrogen receptor
9	781.5	63.5	535	2 S58224	estrogen receptor
10	784.5	62.2	477	2 S71400	estrogen receptor
11	784.5	62.2	530	2 JC5939	estrogen receptor
12	758.5	61.7	574	2 A37197	estrogen receptor
13	750.5	61.0	503	2 JW0046	estrogen receptor
14	626.5	50.9	133	2 S26595	estrogen receptor
15	547.5	44.5	121	2 I67419	estradiol receptor
16	374.5	30.4	433	2 B29345	steroid hormone re
17	354.5	28.8	433	2 S58087	estrogen receptor
18	323	26.3	521	2 A29345	steroid hormone re
19	263.5	21.4	758	2 S60586	glucocorticoid rec
20	248	20.2	930	2 A25923	progesterone recep
21	248	20.2	933	1 QRHUP	progesterone recep
22	246	20.1	923	2 A39596	progesterone recep
23	246	20.0	923	2 I53280	progesterone recep
24	243.5	19.8	467	2 A43781	retinoid-X-recepto
25	243	19.8	786	2 A35466	progesterone recep
26	241.5	19.6	488	2 C41977	retinoid receptor
27	240	19.5	441	2 I50515	retinoid X recepto
28	238.5	19.4	771	2 A54273	glucocorticoid rec
29	236.5	19.2	462	1 S09592	retinoid X recepto

ALIGNMENTS

RESULT 1  
QRHUE

estrogen receptor 1 - human  
N:Alternate names: ER1; estrogen receptor alpha  
C:Species: Homo sapiens (man)  
C:Date: 28-May-1986 #sequence revision 28-May-1986 #text change 09-Jul-2004  
C:Accession: A94284; A93376; A43021; S27143; S34000; A41925; A03244; C41925; D41  
R:Greene, G.L.; Gilna, P.; Waterfield, M.; Baker, A.; Hort, Y.; Shine, J.  
Science 231, 1150-1154, 1986  
A:Title: Sequence and expression of human estrogen receptor complementary DNA.  
A:Reference number: A94284; MUID:86122927; PMID:3753802  
A:Accession: A94284  
A:Molecule type: mRNA  
A:Residues: 1-595 <GR1>  
A:Cross-references: UNIPROT:Q14268; UNIPROT:Q9UB35; GB:M12674; NID:G182192; PIDN:AAAS239  
R:Green, S.; Walter, P.; Kumar, V.; Krust, A.; Bornert, J.M.; Argos, P.; Chambon, P.  
Nature 320, 134-139, 1986  
A:Title: Human oestrogen receptor cDNA: sequence, expression and homology to v-erb-A.  
A:Reference number: A93376; MUID:86146892; PMID:3754034  
A:Accession: A93376  
A:Molecule type: mRNA  
A:Residues: 1-595 <GR2>  
A:Cross-references: GB:X03635; NID:G31233; PIDN:CAA27284.1; PID:G31234  
R:Ponglikitmongkol, M.; Green, S.; Chambon, P.  
EMBO J. 7, 3385-3388, 1988  
A:Title: Genomic organization of the human estrogen receptor gene.  
A:Reference number: A43021; MUID:89091079; PMID:3145193  
A:Accession: A43021  
A:Molecule type: DNA  
A:Residues: 143-161; 205-225; 244-264; 356-374, 'G', 376; 402-422; 447-460, 'P', 462-467; 508-528  
R:Keaveney, M.; Klug, J.; Gannon, F.  
DNA Seq. 2, 347-358, 1992  
A:Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene  
A:Reference number: S27140; MUID:93075998; PMID:1476547  
A:Accession: S27143  
A>Status: preliminary; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-115 <KEA>  
A:Cross-references: EMBL:XG2462; NID:G31201; PIDN:CAA44322.1; PID:G31205  
R:Pfeffer, U.; Fecarotta, E.; Castagnetta, L.; Vidali, G.  
Cancer Res. 53, 741-743, 1993  
A:Title: Estrogen receptor variant messenger RNA lacking exon 4 in estrogen-responsive h  
A:Reference number: S34000; MUID:93133765; PMID:7916651  
A:Accession: S34000  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 216-254, 367-399, 'G', 401-434 <PFE>  
A:Cross-references: EMBL:X73067; NID:G579865; PIDN:CAA51528.1; PID:G939886  
R:Dotzlaw, H.; Alkhalaf, M.; Murphy, L.C.  
Mol. Endocrinol. 6, 773-785, 1992  
A:Title: Characterization of estrogen receptor variant mRNAs from human breast cancers.

30	236	19.2	467	2	S26668	retinoic acid rece
31	236	19.2	467	2	A47278	retinoid X recepto
32	234.5	19.1	463	2	S26670	retinoic acid rece
33	234.5	19.1	463	2	B41727	retinoid-X recepto
34	233.5	19.0	470	2	D41977	retinoid receptor
35	230.5	18.7	777	1	QRHUGA	glucocorticoid rec
36	230.5	18.7	783	1	A25691	glucocorticoid rec
37	229.5	18.7	742	1	QRHUGB	retinoid X recepto
38	227.5	18.5	379	2	I50514	retinoid X recepto
39	224.5	18.3	848	2	JG0194	androgen receptor
40	223	18.1	533	2	S37781	retinoid X recepto
41	222	18.0	410	2	S26669	retinoic acid rece
42	222	18.0	446	2	A34418	H-2 region II bind
43	222	18.0	448	2	D41727	retinoid X recepto
44	222	18.0	451	2	A41651	retinoic acid rece
45	222	18.0	520	2	I84718	RXR-beta1 isoform

A:Reference number: A41925; MUID:922293154; PMID:1603086  
A:Accession: A41925  
A:Molecule type: mRNA  
A:Residues: 1-214; 'ELPTLC' <DOT>  
A:Cross-references: GB:M69297; NID:g182218; PIDN:AAA58462.1; PID:g182219  
A:Experimental source: clone 4; breast cancer  
A:Note: sequence has been revised after extraction from NCBI backbone  
A:Note: the complete sequence of neither the nucleotide nor the protein is shown in this  
A:Note: Sequence extracted from NCBI backbone (NCBIN:106580)  
A:Accession: B41925  
A:Status: significant sequence differences  
A:Molecule type: mRNA  
A:Cross-references: GB:M69296  
A:Experimental source: clone 24; breast cancer  
A:Note: Sequence extracted from NCBI backbone (NCBIN:106597)  
C:Comment: The steroid hormones and their receptors are involved in the regulation of eu  
C:Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly  
complex appears to recognize discrete DNA sequences upstream of transcriptional start site  
C:Genetics:  
A:Cross-references: GDB:119120; OMIM:133430  
A:Map position: 6q25.1-6q25.1  
A:Introns: 151/2; 215/1; 254/1; 366/1; 412/2; 457/1; 518/2  
C:Superfamily: estrogen receptor; erba transforming protein homology  
C:Keywords: DNA binding; nucleus; phosphoprotein; steroid hormone receptor; transcrip  
F:1-120/Domain: amino-terminal <NH2>  
F:121-299/Domain: DNA binding #status predicted <DNA>  
F:183-456/Domain: erba transforming protein homology <ERBA>  
F:185-205/Region: zinc finger CCCC motif  
F:221-245/Region: zinc finger CCCC motif  
F:300-595/Domain: steroid binding #status predicted <STB>  
F:236.305/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 97.4%; Score 1197.5; DB 1; Length 595;  
Best Local Similarity 95.9%; Pred. No. 5.3e-111;  
Matches 236; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY	1	SLALSITADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV	60
DB	305	SLALSITADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV	364
QY	61	PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGWEI	120
DB	365	PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPVKLLFAPNLLLDNRQKCVGWEI	424
QY	121	FDMLLATSRFRMMNLQGEFVCLKSIIILLNGVYTFXXXXXXXEEKDHIHRVLDKIT	180
DB	425	FDMLLATSRFRMMNLQGEFVCLKSIIILLNGVYTF-LSSTLKSLEEKDHIHRVLDKIT	483
QY	181	DTLIHLMKAGLTLOOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEEM	240
DB	484	DTLIHLMKAGLTLOOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEEM	543
QY	241	LDAHRL 246	
DB	544	LDAHRL 549	

RESULT 2  
ORMSE  
estrogen receptor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 06-Mar-1992 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004  
C:Accession: A40061  
R:White, R.; Lees, J.A.; Needham, M.; Ham, J.; Parker, M.  
Mol. Endocrinol. 1, 735-744, 1987  
A:Title: Structural organization and expression of the mouse estrogen receptor.  
A:Reference number: A40061; MUID:91042558; PMID:2484714  
A:Accession: A40061  
A:Molecule type: mRNA  
A:Residues: 1-599 <WHI>  
A:Cross-references: UNIPROT:P19785; GB:M38651; NID:g193179; PIDN:AAA37580.1; PID:g193180  
C:Comment: The steroid hormones and their receptors are involved in the regulation of eu

C:Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly  
complex appears to recognize discrete DNA sequences upstream of transcriptional start site  
C:Superfamily: estrogen receptor; erba transforming protein homology  
C:Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recept  
F:1-183/Domain: amino-terminal <NH2>  
F:184-275/Domain: DNA binding #status predicted <DNA>  
F:187-460/Domain: erba transforming protein homology <ERBA>  
F:187-210/Region: zinc finger CCCC motif  
F:223-245/Region: zinc finger CCCC motif  
F:260-275/Domain: steroid binding #status predicted <STB>  
F:304-556/Domain: steroid binding site: zinc (Cys) #status predicted  
F:189.192.206.209/Binding site: zinc (Cys) #status predicted  
F:225.231.241.244/Binding site: zinc (Cys) (covalent) #status predicted  
F:240.303/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 95.2%; Score 1171.5; DB 1; Length 599;  
Best Local Similarity 93.1%; Pred. No. 2.1e-108;  
Matches 229; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

QY	1	SLALSITADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV	60
DB	309	SPALSITADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV	368
QY	61	PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGWEI	120
DB	369	PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGWEI	428
QY	121	FDMLLATSRFRMMNLQGEFVCLKSIIILLNGVYTFXXXXXXXEEKDHIHRVLDKIT	180
DB	429	FDMLLATSRFRMMNLQGEFVCLKSIIILLNGVYTF-LSSTLKSLEEKDHIHRVLDKIT	487
QY	181	DTLIHLMKAGLTLOOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEEM	240
DB	488	DTLIHLMKAGLTLOOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEEM	547
QY	241	LDAHRL 246	
DB	548	LDAHRL 553	

RESULT 3  
QRTE  
estrogen receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Sep-1991 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004  
C:Accession: S07379; S16731  
R:Koike, S.; Sakai, M.; Muramatsu, M.  
Nucleic Acids Res. 15, 2499-2513, 1987  
A:Title: Molecular cloning and characterization of rat estrogen receptor cDNA.  
A:Reference number: S07379; MUID:87174780; PMID:3031601  
A:Accession: S07379  
A:Molecule type: mRNA  
A:Residues: 1-600 <KOI>  
A:Cross-references: UNIPROT:P06211; EMBL:X00102; NID:g56110; PIDN:CAA68287.1; PID:g56111  
R:Maggi, A.M.A.  
submitted to the EMBL Data Library, June 1991  
A:Reference number: S16731  
A:Accession: S16731  
A:Molecule type: mRNA  
A:Residues: 1-487; 'T', 489-600 <MAG>  
A:Cross-references: EMBL:X61098; NID:g56120; PIDN:CAA43411.1; PID:g56121  
C:Comment: The steroid hormones and their receptors are involved in the regulation of eu  
C:Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly  
complex appears to recognize discrete DNA sequences upstream of transcriptional start site  
C:Superfamily: estrogen receptor; erba transforming protein homology  
C:Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recept  
F:1-184/Domain: amino-terminal <NH2>  
F:185-276/Domain: DNA binding #status predicted <DNA>  
F:188-461/Domain: erba transforming protein homology <ERBA>  
F:188-211/Region: zinc finger CCCC motif  
F:224-246/Region: zinc finger CCCC motif  
F:261-276/Region: nuclear location signal  
F:305-557/Domain: steroid binding #status predicted <STB>

F/300-595/Domain: steroid binding #status predicted <STB>  
F/185.188.202.205/Binding site: zinc (Cys) #status predicted  
F/221.227.237.240/Binding site: zinc (Cys) #status predicted  
F/236.305/Binding site: phosphate (Ser) (covalent) #status predicted

Db	545	NIQGEFVCLKSII	ILLNSGVYFSL	STLSLEEKDHI	HRVLDKITT	TLHLMAKAGITLQ	604
Qy	196	QOQRLAQLLL	TLSHIRMSNKG	MEHLYSMCKQ	VVPLVDLLEML	DAHRL	246

RESULT 6

ORCHE

estrogen receptor - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 06-Mar-1992 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004  
C:Accession: A40914; S07192  
R:Maxwell, B.L.; McDonnell, D.P.; Conneely, O.M.; Schulz, T.Z.; Greene, G.L.; O'Malley, M.L. Endocrinol. 1, 25-35, 1987  
A:Title: Structural organization and regulation of the chicken estrogen receptor.  
A:Reference number: A40914; MUID:88318621; PMID:2901032  
A:Accession: A40914  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-589 <MAX>  
A:Cross-references: UNIPROT:P06212  
R:Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P. EMBO J. 5, 891-897, 1986  
A:Comment: The chicken estrogen receptor sequence: homology with v-erbA and the human oes  
A:Reference number: S07192; MUID:86247578; PMID:3755102  
A:Accession: S07192  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-256, E', 258-589 <KRU>  
A:Cross-references: EMBL:X03805; NID:G63378; PIDN:CAA27433.1; PID:G63380  
C:Comment: The steroid hormones and their receptors are involved in the regulation of eu  
C:Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly  
complex appears to recognize discrete DNA sequences upstream of transcriptional start sit  
C:Superfamily: estrogen receptor; erbA transforming protein homology  
C:Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep  
F:1-173/Domain: amino-terminal <NH2>  
F:174-265/Domain: DNA binding #status predicted <DNA>  
F:177-450/Domain: erbA transforming protein homology <ERBA>  
F:213-235/Region: zinc finger CCCC motif  
F:250-265/Region: nuclear location signal  
F:294-546/Domain: steroid binding #status predicted <STB>  
F:179,182,196,199/Binding site: zinc (Cys) #status predicted  
F:215,221,231,234/Binding site: zinc (Cys) #status predicted  
F:230,299/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 93.0%; Score 1143.5; DB 1; Length 589;  
Best Local Similarity 90.2%; Pred. No. 1.2e-105;  
Matches 222; Conservative 12; Mismatches 11; Indels 1; Gaps 1;  
QY 1 SLALSITADQWVSALLDAPPIIYSEYDPTFPFSEASMMGLLTNLADRELHVMINWAKRV 60  
DB 299 SPALSITAEQWVSALLAEPPIVYSEYDPTFPFSEASMMGLLTNLADRELHVMINWAKRV 358  
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQGKVEGMVEI 120  
DB 359 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQGKVEGMVEI 418  
QY 121 FDMILATSSRFMMNLQGEFFVCLKSIILLNSGVYTFXXXXXXEEDKHHRVLDKIT 180  
DB 419 FDMILATSSRFMMNLQGEFFVCLKSIILLNSGVYTF-LSSSTLSLEEDTDLHIILDKII 477  
QY 181 DTILHLMKAGITLQOQHQRLLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLDYLLLEM 240  
DB 478 DTILHLMKAGITLQOQHQRLLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLDYLLLEM 537  
QY 241 LDAHRL 246  
DB 538 LDAHRL 543

RESULT 7

ORXLE

estrogen receptor - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 28-Feb-1992 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004  
C:Accession: A40907  
estrogen receptor - Oryzias sp. (strain d-rR)  
C:Species: Oryzias sp.  
C:Variety: strain d-rR  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T10423  
R:Okada, H.; Kawahara, T.; Yamashita, I. submitted to the EMBL Data Library, March 1994  
A:Description: Cloning of medaka estrogen receptor cDNA.  
A:Reference number: Z17013  
A:Accession: T10423  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-620 <OKA>  
A:Cross-references: UNIPROT:P50241; EMBL:D28954  
A:Experimental source: strain d-rR, liver  
C:Genetics: MER  
C:Superfamily: estrogen receptor; erbA transforming protein homology  
C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation  
F:184-460/Domain: erbA transforming protein homology <ERB>

Query Match 64.4%; Score 792.5; DB 2; Length 620;  
RESULT 8  
T10423  
estrogen receptor - Oryzias sp. (strain d-rR)  
C:Species: Oryzias sp.  
C:Variety: strain d-rR  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T10423  
R:Okada, H.; Kawahara, T.; Yamashita, I. submitted to the EMBL Data Library, March 1994  
A:Description: Cloning of medaka estrogen receptor cDNA.  
A:Reference number: Z17013  
A:Accession: T10423  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-620 <OKA>  
A:Cross-references: UNIPROT:P50241; EMBL:D28954  
A:Experimental source: strain d-rR, liver  
C:Genetics: MER  
C:Superfamily: estrogen receptor; erbA transforming protein homology  
C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation  
F:184-460/Domain: erbA transforming protein homology <ERB>

R:Weiler, I.J.; Lew, D.; Shapiro, D.J. Mol. Endocrinol. 1, 355-362, 1987  
A:Title: The Xenopus laevis estrogen receptor: sequence homology with human and avian rec  
A:Reference number: A40907; MUID:90331927; PMID:3274894  
A:Accession: A40907  
A:Molecule type: mRNA  
A:Residues: 1-586 <WEI>  
A:Cross-references: UNIPROT:P81559; GB:L20735  
C:Comment: The steroid hormones and their receptors are involved in the regulation of eu  
C:Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly  
complex appears to recognize discrete DNA sequences upstream of transcriptional start site  
C:Superfamily: estrogen receptor; erbA transforming protein homology  
C:Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep  
F:1-174/Domain: amino-terminal <NH2>  
F:175-266/Domain: DNA binding #status predicted <DNA>  
F:178-448/Domain: erbA transforming protein homology <ERBA>  
F:214-237/Region: zinc finger CCCC motif  
F:251-266/Region: nuclear location signal  
F:292-544/Domain: steroid binding #status predicted <STB>  
F:180,183,197,200/Binding site: zinc (Cys) #status predicted  
F:216,222,232,235/Binding site: zinc (Cys) #status predicted  
F:231/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 84.3%; Score 1037.5; DB 1; Length 586;  
Best Local Similarity 80.1%; Pred. No. 4.3e-95;  
Matches 197; Conservative 25; Mismatches 23; Indels 1; Gaps 1;  
QY 1 SLALSITADQWVSALLDAPPIIYSEYDPTFPFSEASMMGLLTNLADRELHVMINWAKRV 60  
DB 297 SPVLSITAEQLISALMEAEAPIVYSEHSTKPLSEASMMGLLTNLADRELHVMINWAKRV 356  
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQGKVEGMVEI 120  
DB 357 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQGKVEGMVEI 416  
QY 121 FDMILATSSRFMMNLQGEFFVCLKSIILLNSGVYTFXXXXXXEEDKHHRVLDKIT 180  
DB 417 FDMILATSSRFMMNLQGEFFVCLKSIILLNSGVYTF-LSSSTLSLEEDTDLHIILDKII 475  
QY 181 DTILHLMKAGITLQOQHQRLLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLDYLLLEM 240  
DB 476 DTILHLMKAGITLQOQHQRLLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLDYLLLEM 535  
QY 241 LDAHRL 246  
DB 536 LDAHRL 541

Query Match 64.4%; Score 792.5; DB 2; Length 620;  
RESULT 8  
T10423  
estrogen receptor - Oryzias sp. (strain d-rR)  
C:Species: Oryzias sp.  
C:Variety: strain d-rR  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T10423  
R:Okada, H.; Kawahara, T.; Yamashita, I. submitted to the EMBL Data Library, March 1994  
A:Description: Cloning of medaka estrogen receptor cDNA.  
A:Reference number: Z17013  
A:Accession: T10423  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-620 <OKA>  
A:Cross-references: UNIPROT:P50241; EMBL:D28954  
A:Experimental source: strain d-rR, liver  
C:Genetics: MER  
C:Superfamily: estrogen receptor; erbA transforming protein homology  
C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation  
F:184-460/Domain: erbA transforming protein homology <ERB>

Best Local Similarity 63.0%, Pred. No. 1.1e-70;	
Matches 155; Conservative 39; Mismatches 43; Indels 9; Gaps 2;	
Qy	5 SLTADQVVSALLDAEPPIIXSEYDTPRFPSEASMMGLLTNLADRELVHMINKAKRVPGFV 64
Db	131 SIPEQVLLLLQGAEPILCSRQKLSRPYTEVTMTILTSWADRELVHTAWAKKPGFL 372
Qy	65 DLTUHQVHLLECWLFIEMTLGLVWRSMHPGKLLFAPNLLDRNQCKVEGVMEIFDML 124
Db	373 QLSLHDQVLLLESWLEVLMIGLIWRGTHCPGLIFAQDLILDRNGDCVEGVMTIEIFDML 432
Qy	125 LATSSRRMMNLQGEFEVCLKSIILLNSGVYTFXXXXXXXEKDH-----IHRVLKTI 180
Db	433 LATASRFVLKLPKEEFVCLKAIILLNSGAFSPCTGTM-----EPLHNSAAVQSMLEDTIT 487
Qy	181 DTILHLMAKAGLTLQOQHORLAQLLLLSLHTRHNSKGMHLYSMKCKNVVPLYLALLEM 240
Db	488 DALIHYSQSGYLAQEQARRQAQLLLLSLHTRHNSKGMHLYSMKCKNVVPLYLALLEM 547
Qy	241 LDAHRL 246
Db	548 LDAHRL 553

RESULT 9  
S58224  
oestrogen receptor - Atlantic salmon (fragment)  
C:Species: Salmo salar (Atlantic salmon)  
C:Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004  
C:Accession: S58224  
R:Rogers, S.A.; Llewellyn, L.; Ramsurn, V.P.; Sweeney, G.E.; Wigham, T.  
submitted to the EMBL Data Library, July 1995  
A:Reference number: S58224  
A:Accession: S58224  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-535 <ROG>  
A:Cross-references: UNIPROT:P50242; EMBL:X89959; NID:g929901; PID:g929901; PID:g929901; PID:CAA61999.1; PID:g929901  
C:Superfamily: estrogen receptor; erba transforming protein homology  
C:Keywords: steroid hormone receptor; zinc finger  
F:103-382/Domain: erba transforming protein homology <ERBA>

Query Match	63.5%	Score	781.5;	DB 2;	Length	535;		
Best Local Similarity	61.7%;	Pred. No.	1.1e-69;					
Matches	150;	Conservative	39;	Mismatches	53;	Indels	1; Gaps	1; Gaps
QY	4	LSUTAOQMSGALLDABPPILYSEYDPTRPESASMGGLTNLADRELVHMHNWAKRVPGF	63					
DB	234	ITMPPEQVFLLOQAEPPALCSRQKVAPYTEVTMTLLTSMADKELVHMVWAKKVPGF	293					
QY	64	VDLTLDQVHLLCEAMLEIIMGLVWRSMEHPGKLLFAPNLLLDNRQCKVCVEGWVIFDM	123					
DB	294	QELSLHDQVQLLESMSLEVLIMGLIWRSHCPGKLIFAQDLILDRSEGDCVEGMAEIFDM	353					
QY	124	LLATSRFRMNIQGEFVCLKSTILLNSGVYTFXXXXXXXEEXDHIHRVLDKTDITDL	183					
DB	354	LLATSRFRMLKLPDEFVCLKAILLNSGAFSF-CSNSVESLHNSAVESMDNITDAL	412					
QY	184	IHLMAKAGLTQOOQHORLAQLLILSHIRHMSKNGMEHLYSMKCKNVVPLYDLLLEMLDA	243					
DB	413	IHHISHSGASVQQPQQVQVQLLLLLSHIRHMSKNGMEHLYSICKKNKVPPLYDLLLEMLDG	472					
QY	244	HLR 246						
DB	473	HLR 475						

```

RESULT 10
S71400
estrogen receptor beta - human
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Jun-2000
C:Accession: S71400

```

R.Moselman, S.; Polman, J.; Dijkema, R.  
FEBS Lett. 392, 49-53, 1996  
A;Title: ER-beta: identification and characterization of a novel human estrogen receptor  
C;Superfamily: DNA binding site: phosphoprotein; steroid hormone recep  
P:94-355/DNA;Domain: erba transforming protein homology <ERBA>  
F:96-116/Region: zinc finger CCCC motif  
E:132-156/Region: zinc finger CCCC motif  
F:167-182/Region: nuclear location signal  
F:52/Binding site: phosphate (Ser) #status predicted  
F:96\_99\_113\_116/Binding site: zinc (Cys) #status predicted  
F:132,138,148,151/Binding site: zinc (Cys) #status predicted

Query Match      62.2%; Score 764.5; DB 2; Length 477;  
Best Local Similarity    59.3%; Pred. No. 4.8e+68;  
Matches 144; Conservative 52; Mismatches 42; Indels 5; Gaps 3;

Qy         5 SLTADQMVSALLDABPP--ILYSEYPDTRPFSEASMMGLLTNLADRDLVHMNWKAKVPGF    63  
                :|::||:|||||:|::||::||| |::||| |||||:||||:  
Db         209 ALSPEQLVLTLLEAPPHVLSR--PSAPTFTSMMMSITKLADKELVHWSWKKIPGP    266  
  
Qy         64 VDLTHDOHVLLCAWLBEIMIGLVWRSMHGPKLLFAPNLLLDRNQGKCVEGMVFDM    123  
Db         267 VELSLFDQVRLLSCWMEVLMMLMWSRIDHPKLIIFAPDLVLDREGKCVGEIILEIFDM    326  
  
Qy         124 LLATSSRRFRMNLOGEEFCVKLSIIILLNSGVYTFEXXXXXXXEEKDHIRVLDTLTDYL    183  
Db         327 LLATTSRPRFLQHKECYLCVKAMILLNSSMYPLVTATODASSRK--LAHLLNNAVVDAL    384  
  
Qy         184 IHLMAKAGLTQQOQRIOQAULLILLSHRHSNMKGHELYSMCKKNWPPLYDLLLEMLDA    243  
Db         385 VWVTAKSGISSQQSQMRLANLLMLLSHYRHASKMGHEHLNNMKCNVFPDYDLLEMLNA    444  
  
Qy         244 HRL    246  
Db         445 HVL    447

RESULT 11  
JC5939  
estrogen receptor beta - human  
C;Species: Homo sapiens (man)  
C;Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 21-Jul-2000  
C;Accession: JC5939  
R;Osawa, S.; Inoue, S.; Watanabe, T.; Hiroi, H.; Orimo, A.; Hosoi, T.; Ouchi, Y.; Muramat  
Biochem. Biophys. Res. Commun. 243, 122-126, 1998  
A;Title: The complete primary structure of human estrogen receptor beta (herbeta) and its  
A;Reference number: JC5939; PMID:98139878; PMID:9473491  
A;Accession: JC5939  
A>Status: preliminary  
A:Molecule type: mRNA  
A;Residues: 1-530 <OGA>  
A;Cross-references: DDJ:AB006590; NID:g2911151; PID:BAA24953.1; PID:g2911152  
C;Superfamily: estrogen receptor; erba transforming protein homology  
F:147-408/Domain: erba transforming protein homology <ERR>

RESULT 11  
JC5939  
estrogen receptor beta - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 21-Jul-2000  
C:Accession: JC5939  
R:Ogawa, S.; Inoue, S.; Watanabe, T.; Hiroi, H.; Orimo, A.; Hosoi, T.; Ouchi, Y.; Muramat  
Biochem. Biophys. Res. Commun. 243, 122-126, 1998  
A:Title: The complete primary structure of human estrogen receptor beta (hERbeta) and its  
A:Reference number: JC5939; MUID:98139878; PMID:9473491  
A:Accession: JC5939  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-530 <OGA>  
A:Cross-references: DDBJ:AB006590; NID:G2911151; PID:G2911152  
C:Superfamily: estrogen receptor; erba transforming protein homology  
F:147-408/Domain: erba transforming protein homology <ERB>

	Query Match	62.2%	Score 764.5;	DB 2;	Length 530;
	Best Local Similarity	59.3%;	Pred. NO. 5.5e-68;		
	Matches 144; Conservative	52;	Mismatches 48;	Indels 5;	Gaps 3;
Qy	5 SLTADQMVSALLDAEPP--ILYSEVDPTPFSEASMMGLLTNLADRELVHNMWAKRVPGF	63			
	: :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :				
Dd	262 ALSPEQLVLTLAEAPHVLISR--PSAPFTFEASMMGLTKUADRELVHNIISWAKIPGF	319			
	: :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :				
Qy	64 VDLTLHDQVHLLECAWLIEILMIGLWVRSMERHPGKLLFAPNLLLDNRNQGVCEGMVBI FDM	123			
	: :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :				
Dd	320 VELSLFDQVRLLESCEWMEVLMGLMWRSIDHPGKLI FAPDLVLDREGKCVGEILEIFDM	379			
	: :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :  : :				



C;Species: Macaca mulatta (rhesus macaque)  
 C;Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 09-Jul-2004  
 C;Accession: I67419  
 R;Chandrasekhar, Y.A.; Melner, M.H.; Nagalla, S.R.; Stouffer, R.L.  
 Endocrinology 135, 307-314, 1994  
 A;Title: Progesterone receptor, but not estradiol receptor, messenger ribonucleic acid  
 A;Reference number: 153287; MUID:94283272; PMID:8013365  
 A;Accession: I67419  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-121 <RES>  
 A;Cross-references: UNIPROT:P49886; GB:S71040; NID:G547182; PIDN:AAB31102.1; PID:G547183  
 C;Superfamily: estrogen receptor; erba transforming protein homology  
 C;Keywords: steroid hormone receptor; zinc finger  
 F;1-54/Domain: erba transforming protein homology (fragment) <ERBA>

Query Match 44.5%; Score 547.5; DB 2; Length 121;  
 Best Local Similarity 91.0%; Pred. No. 3.5e-47;  
 Matches 111; Conservative 1; Mismatches 9; Indels 1; Gaps 1;  
 Qy 99 LFAPNLLDRNQKCVGMEIFDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTFX 158  
 Db 1 LFAPNLLDRNQKCVGMEIFDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF- 59  
 Qy 159 XXXXXXKXKDHHRVLDKITDTLIHLMKAGLTLOQQRRLAQLLLILSHIRHMSNKG 218  
 Db 60 LSSTLKSLEKDHHRVLDKITDTLIHLMKAGLTLOQQRRLAQLLLILSHIRHMSNKG 119  
 Qy 219 ME 220  
 Db 120 ME 121

Search completed: November 8, 2004, 08:28:28  
 Job time : 12.049 secs

*This Page Blank (usntn)*



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2004, 08:28:04 ; Search time 37.151 Seconds  
(without alignments)  
2338.928 Million cell updates/sec

Title: US-09-830-693B-28

Perfect score: 1230

Sequence: 1 SLALSITADQMSALLDAEP.....CKNVVPLYDLLEMLDAHRL 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Top 10 number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09D\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10F\_PUBCOMB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US10G\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US10H\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1206.5	98.1	414	14	US-10-157-899A-2
2	1206.5	98.1	438	14	US-10-157-899A-4
3	1206.5	98.1	595	9	US-09-853-033-2
4	1206.5	98.1	595	14	US-10-148-835-1
5	1206.5	98.1	595	14	US-10-148-835-2
6	1206.5	98.1	595	14	US-10-148-835-9
7	1202.5	97.8	595	14	US-10-148-835-5
8	1200.5	97.6	595	14	US-10-148-835-3
9	1199.5	97.5	595	14	US-10-148-835-4
10	1199.5	97.5	595	14	US-10-148-835-10
11	1198.5	97.4	595	14	US-10-148-835-8
12	1198.5	97.4	660	9	US-09-853-033-4
13	1197.5	97.4	414	14	US-10-157-899A-8

Sequence 14, Appl	14	1197.5	97.4	438	14	US-10-157-899A-14	Sequence 14, Appl
Sequence 19, Appl	15	1197.5	97.4	511	14	US-10-006-760-19	Sequence 19, Appl
Sequence 10, Appl	16	1197.5	97.4	547	14	US-10-052-092-10	Sequence 10, Appl
Sequence 10, Appl	17	1197.5	97.4	547	14	US-10-437-107-10	Sequence 10, Appl
Sequence 17, Appl	18	1197.5	97.4	591	14	US-10-278-481-17	Sequence 17, Appl
Sequence 2, Appl	19	1197.5	97.4	595	9	US-09-933-267A-2	Sequence 2, Appl
Sequence 10, Appl	20	1197.5	97.4	595	10	US-09-952-680A-10	Sequence 10, Appl
Sequence 1, Appl	21	1197.5	97.4	595	13	US-10-096-710-1	Sequence 1, Appl
Sequence 2, Appl	22	1197.5	97.4	595	13	US-10-081-563-2	Sequence 2, Appl
Sequence 9, Appl	23	1197.5	97.4	595	14	US-10-052-092-9	Sequence 9, Appl
Sequence 13, Appl	24	1197.5	97.4	595	14	US-10-052-092-13	Sequence 13, Appl
Sequence 14, Appl	25	1197.5	97.4	595	14	US-10-052-092-14	Sequence 14, Appl
Sequence 61, Appl	26	1197.5	97.4	595	14	US-10-207-655-61	Sequence 61, Appl
Sequence 128, Appl	27	1197.5	97.4	595	14	US-10-177-293-128	Sequence 128, Appl
Sequence 55, Appl	28	1197.5	97.4	595	14	US-10-157-899A-55	Sequence 55, Appl
Sequence 9, Appl	29	1197.5	97.4	595	14	US-10-437-107-9	Sequence 9, Appl
Sequence 11, Appl	30	1197.5	97.4	595	14	US-10-437-107-13	Sequence 11, Appl
Sequence 14, Appl	31	1197.5	97.4	595	14	US-10-437-107-14	Sequence 14, Appl
Sequence 2, Appl	32	1197.5	97.4	595	14	US-10-095-373A-2	Sequence 2, Appl
Sequence 6, Appl	33	1197.5	97.4	595	14	US-10-392-274-2	Sequence 6, Appl
Sequence 7, Appl	34	1197.5	97.4	595	14	US-10-148-835-7	Sequence 7, Appl
Sequence 42, Appl	35	1197.5	97.4	595	14	US-10-148-835-6	Sequence 42, Appl
Sequence 73, Appl	36	1197.5	97.4	595	14	US-10-144-198-42	Sequence 73, Appl
Sequence 69, Appl	37	1197.5	97.4	676	14	US-10-095-373A-73	Sequence 69, Appl
Sequence 71, Appl	38	1197.5	97.4	726	14	US-10-095-373A-71	Sequence 71, Appl
Sequence 67, Appl	39	1197.5	97.4	727	14	US-10-095-373A-67	Sequence 67, Appl
Sequence 10, Appl	40	1197.5	97.4	727	14	US-10-095-373A-10	Sequence 10, Appl
Sequence 16, Appl	41	1196.5	97.3	414	14	US-10-157-899A-16	Sequence 16, Appl
Sequence 8, Appl	42	1196.5	97.3	438	14	US-09-853-033-8	Sequence 8, Appl
Sequence 10, Appl	43	1195.5	97.2	660	9	US-09-853-033-10	Sequence 10, Appl
Sequence 6, Appl	44	1194.5	97.1	242	15	US-10-355-218-10	Sequence 6, Appl
	45	1192.5	97.0	414	14	US-10-157-899A-6	

## ALIGNMENTS

### RESULT 1

US-10-157-899A-2  
; Sequence 2, Application US/10157899A  
; Publication No. US20030143559A1  
; GENERAL INFORMATION:  
; APPLICANT: Bracken, Kathryn Rene  
; APPLICANT: de los Angeles, Joseph Ernest  
; APPLICANT: Huang, Ying  
; APPLICANT: Kadan, Michael Joseph  
; APPLICANT: Keander, Gary Michael  
; APPLICANT: Zerby, Dennis  
; TITLE OF INVENTION: NOVEL ESTROGEN RECEPTOR LIGAND BINDING DOMAIN VARIANTS AND NOVEL  
; TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS  
; FILE REFERENCE: 4-32018A  
; CURRENT APPLICATION NUMBER: US/10157,899A  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 60/294,839  
; PRIOR FILING DATE: 2001-05-31  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 414  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fusion of the human-Estrogen-receptor-ligand-binding-domain and a  
; OTHER INFORMATION: zinc finger array (C7)  
US-10-157-899A-2

Query Match 98.1%; Score 1206.5; DB 14; Length 414;  
Best Local Similarity 96.3%; Pred. No. 2.2e-125;  
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 1 SLALSITADQMSALLDAEPPILYSEYDPTPTPSEASMGGLTTLADRELVHMINAKRV 60

Db 122 SLALSITADQMSALLDAEPPILYSEYDPTPTPSEASMGGLTTLADRELVHMINAKRV 181

QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 120  
DB 182 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 241  
QY 121 FDMLLATSRFRMNLQGEFVCLSIILLNSGVYTFXXXXXXXKDHHRVLDKIT 180  
DB 242 FDMLLATSRFRMNLQGEFVCLSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 300  
QY 181 DTLIHLMAKAGTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 120  
DB 301 DTLIHLMAKAGTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 241  
QY 241 LDAHRL 246  
DB 361 LDAHRL 366

RESULT 2  
US-157-899A-4  
; Sequence 4, Application US/10157899A  
; Patent No. US20030143559A1  
; GENERAL INFORMATION:  
; APPLICANT: Bracken, Kathryn Rene  
; APPLICANT: de los Angeles, Joseph Ernest  
; APPLICANT: Huang, Ying  
; APPLICANT: Kadan, Michael Joseph  
; APPLICANT: Ksander, Gary Michael  
; APPLICANT: Zerby, Dennis  
; TITLE OF INVENTION: NOVEL ESTROGEN RECEPTOR LIGAND BINDING DOMAIN VARIANTS AND NOVEL  
; FILE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS  
; FILE REFERENCE: 4-32018A  
; CURRENT APPLICATION NUMBER: US/10/157,899A  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 60/294,839  
; PRIOR FILING DATE: 2001-05-31  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 438  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fusion of the human-Estrogen-receptor-ligand-binding-domain and a  
; OTHER INFORMATION: zinc finger array(C7)  
US-10-157-899A-4

Query Match 98.1%; Score 1206.5; DB 14; Length 438;  
Best Local Similarity 96.3%; Pred. No. 2.4e-125;  
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
QY 1 SLALSITADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 146 SLALSITADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 205  
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 120  
DB 206 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 265  
QY 121 FDMLLATSRFRMNLQGEFVCLSIILLNSGVYTFXXXXXXXKDHHRVLDKIT 180  
DB 266 FDMLLATSRFRMNLQGEFVCLSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 324  
QY 181 DTLIHLMAKAGTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 120  
DB 325 DTLIHLMAKAGTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 384  
QY 241 LDAHRL 246  
DB 385 LDAHRL 390

RESULT 3

US-09-853-033-2  
; Sequence 2, Application US/09853033  
; Patent No. US20020100068A1  
; GENERAL INFORMATION:  
; APPLICANT: CHAMBEON, PIERRE  
; APPLICANT: METZGER, DANIEL  
; TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION  
; FILE OF INVENTION: MEDIATED BY MODIFIED CRE-ER  
; FILE REFERENCE: 065691/0222  
; CURRENT APPLICATION NUMBER: US/09/853,033  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: FR 00/12570  
; PRIOR FILING DATE: 2000-10-03  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 595  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-853-033-2

Query Match 98.1%; Score 1206.5; DB 9; Length 595;  
Best Local Similarity 96.3%; Pred. No. 3.5e-125;  
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
QY 1 SLALSITADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 305 SLALSITADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364  
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 120  
DB 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 424  
QY 121 FDMLLATSRFRMNLQGEFVCLSIILLNSGVYTFXXXXXXXKDHHRVLDKIT 180  
DB 425 FDMLLATSRFRMNLQGEFVCLSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483  
QY 181 DTLIHLMAKAGTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 240  
DB 484 DTLIHLMAKAGTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 543  
QY 241 LDAHRL 246  
DB 544 LDAHRL 549

RESULT 4  
US-10-148-835-1  
; Sequence 1, Application US/10148835  
; Publication No. US20030207380A1  
; GENERAL INFORMATION:  
; APPLICANT: SAITO et al.  
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION  
; FILE REFERENCE: 2185-0648P  
; CURRENT APPLICATION NUMBER: US/10/148,835  
; CURRENT FILING DATE: 2002-10-11  
; NUMBER OF SEQ ID NOS: 213  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 595  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-148-835-1

Query Match 98.1%; Score 1206.5; DB 14; Length 595;  
Best Local Similarity 96.3%; Pred. No. 3.5e-125;  
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
QY 1 SLALSITADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 305 SLALSITADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364  
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 120

```
Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 424
Qy 121 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180
Db 425 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483
Qy 181 DTLIHLMKAGLTQQOQHRLAQQLLLSHIRHMSNKGMEHLYSMCKKNVVPVLDLLEM 240
Db 484 DTLIHLMKAGLTQQOQHRLAQQLLLSHIRHMSNKGMEHLYSMCKKNVVPVLDLLEM 543
Qy 241 LDAHRL 246
Db 544 LDAHRL 549

RESULT 5
US-10-148-835-2
; Sequence 2, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-2

Query Match 98.1%; Score 1206.5; DB 14; Length 595;
Best Local Similarity 96.3%; Pred. No. 3.5e-125;
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 1 SLALSLTADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 120
Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 424
Qy 121 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180
Db 425 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483
Qy 181 DTLIHLMKAGLTQQOQHRLAQQLLLSHIRHMSNKGMEHLYSMCKKNVVPVLDLLEM 240
Db 484 DTLIHLMKAGLTQQOQHRLAQQLLLSHIRHMSNKGMEHLYSMCKKNVVPVLDLLEM 543
Qy 241 LDAHRL 246
Db 544 LDAHRL 549

RESULT 6
US-10-148-835-9
; Sequence 9, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-9

Query Match 98.1%; Score 1206.5; DB 14; Length 595;
Best Local Similarity 96.3%; Pred. No. 3.5e-125;
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 1 SLALSLTADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 120
Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 424
Qy 121 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180
Db 425 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483
Qy 181 DTLIHLMKAGLTQQOQHRLAQQLLLSHIRHMSNKGMEHLYSMCKKNVVPVLDLLEM 240
Db 484 DTLIHLMKAGLTQQOQHRLAQQLLLSHIRHMSNKGMEHLYSMCKKNVVPVLDLLEM 543
Qy 241 LDAHRL 246
Db 544 LDAHRL 549

RESULT 7
US-10-148-835-5
; Sequence 5, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-5

Query Match 97.8%; Score 1202.5; DB 14; Length 595;
Best Local Similarity 95.9%; Pred. No. 9.9e-125;
Matches 236; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

Qy 1 SLALSLTADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 120
Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 424
Qy 121 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180
Db 425 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483
Qy 181 DTLIHLMKAGLTQQOQHRLAQQLLLSHIRHMSNKGMEHLYSMCKKNVVPVLDLLEM 240
Db 484 DTLIHLMKAGLTQQOQHRLAQQLLLSHIRHMSNKGMEHLYSMCKKNVVPVLDLLEM 543
Qy 241 LDAHRL 246
Db 544 LDAHRL 549

RESULT 8
```

```
Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 424
Qy 121 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180
Db 425 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483
Qy 181 DTLIHLMKAGLTQQOQHRLAQQLLLSHIRHMSNKGMEHLYSMCKKNVVPVLDLLEM 240
Db 484 DTLIHLMKAGLTQQOQHRLAQQLLLSHIRHMSNKGMEHLYSMCKKNVVPVLDLLEM 543
Qy 241 LDAHRL 246
Db 544 LDAHRL 549

RESULT 5
US-10-148-835-2
; Sequence 2, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-2

Query Match 98.1%; Score 1206.5; DB 14; Length 595;
Best Local Similarity 96.3%; Pred. No. 3.5e-125;
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 1 SLALSLTADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 120
Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 424
Qy 121 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180
Db 425 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483
Qy 181 DTLIHLMKAGLTQQOQHRLAQQLLLSHIRHMSNKGMEHLYSMCKKNVVPVLDLLEM 240
Db 484 DTLIHLMKAGLTQQOQHRLAQQLLLSHIRHMSNKGMEHLYSMCKKNVVPVLDLLEM 543
Qy 241 LDAHRL 246
Db 544 LDAHRL 549

RESULT 6
US-10-148-835-9
; Sequence 9, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-9

Query Match 98.1%; Score 1206.5; DB 14; Length 595;
Best Local Similarity 96.3%; Pred. No. 3.5e-125;
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 1 SLALSLTADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 120
Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 424
Qy 121 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180
Db 425 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483
Qy 181 DTLIHLMKAGLTQQOQHRLAQQLLLSHIRHMSNKGMEHLYSMCKKNVVPVLDLLEM 240
Db 484 DTLIHLMKAGLTQQOQHRLAQQLLLSHIRHMSNKGMEHLYSMCKKNVVPVLDLLEM 543
Qy 241 LDAHRL 246
Db 544 LDAHRL 549

RESULT 7
US-10-148-835-5
; Sequence 5, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-5

Query Match 97.8%; Score 1202.5; DB 14; Length 595;
Best Local Similarity 95.9%; Pred. No. 9.9e-125;
Matches 236; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

Qy 1 SLALSLTADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
Db 305 SLALSLTADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 120
Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNOGKCVGMEI 424
Qy 121 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRVLDKIT 180
Db 425 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483
Qy 181 DTLIHLMKAGLTQQOQHRLAQQLLLSHIRHMSNKGMEHLYSMCKKNVVPVLDLLEM 240
Db 484 DTLIHLMKAGLTQQOQHRLAQQLLLSHIRHMSNKGMEHLYSMCKKNVVPVLDLLEM 543
Qy 241 LDAHRL 246
Db 544 LDAHRL 549

RESULT 8
```



Query Match 97.4%; Score 1198.5; DB 14; Length 595;  
Best Local Similarity 95.5%; Pred. No. 2.8e-124;  
Matches 235; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 SLALSLTADQVMSALLDAEPPIYSEYDPTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 305 SLALSLTADQVMSALLDAEPPIYSEYDPTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364

QY 61 PGFVDLTLDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQCCKVEGMVEI 120  
DB 365 PGFVDLTLDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQCCKVEGMVEI 424

QY 121 FDMLLATSSFRMNLQGEFVCLKSIILLNSGYVTF-LSSTLKSLEKDHHRVLDKIT 180  
DB 425 FDMLLATSSFRMNLQGEFVCLKSIILLNSGYVTF-LSSTLKSLEKDHHRVLDKIT 483

QY 181 DTLIHLMAKAGLTQQQHQRQAQLLLSHIRHMSNKGMEHLYSMCKCNVVPVLYDLLEMM 240  
DB 484 DTLIHLMAKAGLTQQQHQRQAQLLLSHIRHMSNKGMEHLYSMCKCNVVPVLYDLLEMM 543

QY 241 LDAHRL 246  
DB 544 LDAHRL 549

RESULT 12  
US-09-853-033-4  
; Sequence 4, Application US/09853033  
; Patent No. US20020100068A1  
; GENERAL INFORMATION:  
; APPLICANT: CHAMBER, PIERRE  
; APPLICANT: METZGER, DANIEL  
; TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION  
; TITLE OF INVENTION: MEDIATED BY MODIFIED CRE-ER  
; FILE REFERENCE: 065691/0222  
; CURRENT APPLICATION NUMBER: US/09/853.033  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: FR 00/12570  
; PRIOR FILING DATE: 2000-10-03  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 660  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric sequence  
; OTHER INFORMATION: Homosapiens-Bacteriophage P1

US-09-853-033-4

Query Match 97.4%; Score 1198.5; DB 9; Length 660;  
Best Local Similarity 95.9%; Pred. No. 3.2e-124;  
Matches 236; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1 SLALSLTADQVMSALLDAEPPIYSEYDPTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 370 SLALSLTADQVMSALLDAEPPIYSEYDPTPRPFSEASMMGLLTNLADRELVHMINWAKRV 429

QY 61 PGFVDLTLDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQCCKVEGMVEI 120  
DB 430 PGFVDLTLDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQCCKVEGMVEI 489

QY 121 FDMLLATSSFRMNLQGEFVCLKSIILLNSGYVTF-LSSTLKSLEKDHHRVLDKIT 180  
DB 490 FDMLLATSSFRMNLQGEFVCLKSIILLNSGYVTF-LSSTLKSLEKDHHRVLDKIT 548

QY 181 DTLIHLMAKAGLTQQQHQRQAQLLLSHIRHMSNKGMEHLYSMCKCNVVPVLYDLLEMM 240  
DB 549 DTLIHLMAKAGLTQQQHQRQAQLLLSHIRHMSNKGMEHLYSMCKCNVVPVLYDLLEMM 608

QY 241 LDAHRL 246  
DB 609 LDAHRL 614

RESULT 13  
US-10-157-899A-8  
; Sequence 8, Application US/10157899A  
; Publication No. US20030143559A1  
; GENERAL INFORMATION:  
; APPLICANT: Bracken, Kathryn Rene  
; APPLICANT: de los Angeles, Joseph Ernest  
; APPLICANT: Huang, Ying  
; APPLICANT: Kadan, Michael Joseph  
; APPLICANT: Ksander, Gary Michael  
; APPLICANT: Zerby, Dennis  
; TITLE OF INVENTION: NOVEL ESTROGEN RECEPTOR LIGAND BINDING DOMAIN VARIANTS AND NOVEL  
; TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS  
; FILE REFERENCE: 4-32018A  
; CURRENT APPLICATION NUMBER: US/10/157,899A  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 60/294,839  
; PRIOR FILING DATE: 2001-05-31  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 414  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fusion of a mutated human-Estrogen-receptor-ligand-binding-domain  
; OTHER INFORMATION: and a zinc finger array (C7)

US-10-157-899A-8

Query Match 97.4%; Score 1197.5; DB 14; Length 414;  
Best Local Similarity 95.5%; Pred. No. 2.2e-124;  
Matches 235; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

QY 1 SLALSLTADQVMSALLDAEPPIYSEYDPTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 122 SLALSLTADQVMSALLDAEPPIYSEYDPTPRPFSEASMMGLLTNLADRELVHMINWAKRV 181

QY 61 PGFVDLTLDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQCCKVEGMVEI 120  
DB 182 PGFVDLTLDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQCCKVEGMVEI 241

QY 121 FDMLLATSSFRMNLQGEFVCLKSIILLNSGYVTF-LSSTLKSLEKDHHRVLDKIT 180  
DB 242 FDMLLATSSFRMNLQGEFVCLKSIILLNSGYVTF-LSSTLKSLEKDHHRVLDKIT 300

QY 181 DTLIHLMAKAGLTQQQHQRQAQLLLSHIRHMSNKGMEHLYSMCKCNVVPVLYDLLEMM 240  
DB 301 DTLIHLMAKAGLTQQQHQRQAQLLLSHIRHMSNKGMEHLYSMCKCNVVPVLYDLLEMM 360

QY 241 LDAHRL 246  
DB 361 LDAHRL 366

RESULT 14  
US-10-157-899A-14  
; Sequence 14, Application US/10157899A  
; Publication No. US20030143559A1  
; GENERAL INFORMATION:  
; APPLICANT: Bracken, Kathryn Rene  
; APPLICANT: de los Angeles, Joseph Ernest  
; APPLICANT: Huang, Ying  
; APPLICANT: Kadan, Michael Joseph  
; APPLICANT: Ksander, Gary Michael  
; APPLICANT: Zerby, Dennis  
; TITLE OF INVENTION: NOVEL ESTROGEN RECEPTOR LIGAND BINDING DOMAIN VARIANTS AND NOVEL  
; TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS  
; FILE REFERENCE: 4-32018A  
; CURRENT APPLICATION NUMBER: US/10/157,899A  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 60/294,839

;  
; PRIOR FILING DATE: 2001-05-31  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 438  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fusion of a mutated human-Estrogen-receptor-ligand-binding-domain  
; OTHER INFORMATION: and a zinc finger array (C7)  
US-10-157-899A-14

Query Match 97.4%; Score 1197.5; DB 14; Length 438;  
Best Local Similarity 95.9%; Pred. No. 2.4e-124; Mismatches 9; Indels 1; Gaps 1;  
Matches 235; Conservative 1;  
QY 1 SLALSITADQVMSALDAPPPILYSEYDTPRPSEASMMGLLTNLADRELVHMINWAKRV 60  
Db 146 SLALSITADQVMSALDAPPPILYSEYDTPRPSEASMMGLLTNLADRELVHMINWAKRV 205  
QY 61 PGFVDLTLDQVHLLFCAMLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGVMVEI 120  
Db 206 PGFVDLTLDQVHLLFCAMLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGVMVEI 265  
QY 121 FDMLLATSSRFPMNMQGEEFVCLKSIILLNSGVYTFEXXXXXXXEEXKHHRVLDKIT 180  
Db 266 FDMALATSSRFPMNMQGEEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 324  
QY 181 DTLIHLMAKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPYDILLEM 240  
Db 325 DTLIHLMAKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPYDILLEM 384  
QY 241 LDAHRL 246  
Db 385 LDAHRL 390

RESULT 15  
US-10-006-760-19  
; Sequence 19, Application US/10006760  
; Publication No. US20030186385A1  
; GENERAL INFORMATION:  
; APPLICANT: Koide, Shohai  
; TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND  
; FILE REFERENCE: 176/60901  
; CURRENT APPLICATION NUMBER: US/10/006,760  
; PRIOR FILING DATE: 2001-11-19  
; OR APPLICATION NUMBER: 60/249,756  
; OR FILING DATE: 2000-11-17  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 511  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: LexA-ER(alpha)EF fusion protein  
US-10-006-760-19

Query Match 97.4%; Score 1197.5; DB 14; Length 511;  
Best Local Similarity 95.9%; Pred. No. 2.9e-124; Mismatches 9; Indels 1; Gaps 1;  
Matches 236; Conservative 0;  
QY 1 SLALSITADQVMSALDAPPPILYSEYDTPRPSEASMMGLLTNLADRELVHMINWAKRV 60  
Db 221 SLALSITADQVMSALDAPPPILYSEYDTPRPSEASMMGLLTNLADRELVHMINWAKRV 280  
QY 61 PGFVDLTLDQVHLLFCAMLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGVMVEI 120  
Db 281 PGFVDLTLDQVHLLFCAMLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGVMVEI 340

QY 121 FDMLLATSSRFPMNMQGEEFVCLKSIILLNSGVYTFEXXXXXXXEEXKHHRVLDKIT 180  
Db 341 FDMLLATSSRFPMNMQGEEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 399  
QY 181 DTLIHLMAKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPYDILLEM 240  
Db 400 DTLIHLMAKAGLTQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPYDILLEM 459  
QY 241 LDAHRL 246  
Db 460 LDAHRL 465

Search completed: November 8, 2004, 08:42:50  
Job time : 38.151 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2004, 08:16:47 ; Search time 14.5592 Seconds  
(without alignments)  
1120.546 Million cell updates/sec

Title: US-09-830-693B-28

Perfect score: 1230

Sequence: 1 SLALSITADQMSALLDAEP.....CKNVVPLYDLLEMLDAHRL 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1206.5	98.1	595	3	US-08-764-870-12
2	1206.5	98.1	595	3	US-08-980-115-12
3	1197.5	97.4	595	2	US-08-836-620A-17
4	1197.5	97.4	595	3	US-09-041-886-35
5	1197.5	97.4	595	4	US-08-453-998-2
6	1197.5	97.4	651	3	US-08-693-940-3
7	1197.5	97.4	651	4	US-09-566-660-3
8	1197.5	97.4	773	3	US-08-564-264-1
9	1180	95.9	410	6	5223606-5
10	1167.5	94.9	596	2	US-08-836-620A-16
11	1146	93.2	264	4	US-09-660-979-1
12	961.5	78.2	243	2	US-08-836-620A-10
13	951.5	77.4	243	2	US-08-836-620A-9
14	946.5	77.0	243	2	US-08-836-620A-8
15	792.5	64.4	575	4	US-09-893-666A-2
16	769.5	62.6	484	2	US-08-836-620A-13
17	769.5	62.6	485	2	US-08-836-620A-2
18	764.5	62.2	477	4	US-09-608-088-5
19	764.5	62.2	477	4	US-09-711-288-5
20	764.5	62.2	485	2	US-08-836-620A-3
21	764.5	62.2	530	4	US-09-608-088-25
22	764.5	62.2	530	4	US-09-711-288-25
23	764.5	62.2	548	3	US-09-139-617-1
24	764.5	62.2	548	4	US-09-561-741A-1
25	764.5	62.2	548	4	US-09-558-795-1
26	757.5	61.6	484	2	US-08-836-620A-14
27	757.5	61.6	485	2	US-08-836-620A-5

Sequence 4, Appli  
Sequence 4, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 7, Appli  
Sequence 15, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 21, Appli  
Sequence 21, Appli  
Sequence 5, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 4, Appli  
Sequence 19, Appli  
Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-08-764-870-12  
; Sequence 12, Application US/08764870  
; Patent No. 6236946  
; GENERAL INFORMATION:  
; APPLICANT: Scanlan, Thomas S  
; APPLICANT: Baxter, John D  
; APPLICANT: Fletterick, Robert J  
; APPLICANT: Wagner, Richard L  
; APPLICANT: Kushner, Peter J  
; APPLICANT: Aprelatti, James W  
; APPLICANT: West, Brian  
; TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Cooley Godward  
; STREET: Five Palo Alto Square, 3000 El Camino Real  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/764,870  
; FILING DATE: 13-DEC-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/008,540  
; FILING DATE: 13-DEC-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/008,543  
; FILING DATE: 13-DEC-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/008,606  
; FILING DATE: 14-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nakamura, Jackie N  
; REGISTRATION NUMBER: 35,966  
; REFERENCE/DOCKET NUMBER: UCAL-246/01US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650)843-5000  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 595 amino acids  
; TYPE: amino acid

```

; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-764-870-12

Query Match      98.1%; Score 1206.5; DB 3; Length 595;
Best Local Similarity 96.3%; Pred. No. 3.1e-134;
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 SLALSTADQMSVALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
DB 305 SLALSTADQMSVALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 120
DB 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 424
QY 121 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXKXKXKHHRVLDKIT 180
DB 425 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLKXKXKHHRVLDKIT 483
QY 181 DTLIHMAKAGTLQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEM 240
DB 484 DTLIHMAKAGTLQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEM 543
QY 241 LDAHRL 246
DB 544 LDAHRL 549

RESULT 3
US-08-836-620A-17
; Sequence 17, Application US/08836620A
; Patent No. 5958710
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Orphan receptor
; NUMBER OF SEQUENCES: 19
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,620A
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/03933
; FILING DATE:
; APPLICATION NUMBER: GB 9518272.1
; FILING DATE: 08-SEP-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: GB 9605550.4
; FILING DATE: 15-MAR-1996
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: GB 9607532.0
; FILING DATE: 11-APR-1996
; APPLICATION NUMBER: GB 9609576.5
; FILING DATE: 08-MAY-1996
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-836-620A-17

Query Match      97.4%; Score 1197.5; DB 2; Length 591;
Best Local Similarity 95.9%; Pred. No. 3.6e-133;
Matches 236; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1 SLALSTADQMSVALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60
DB 305 SLALSTADQMSVALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 120
DB 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEI 424
QY 121 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXKXKXKHHRVLDKIT 180
DB 425 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLKXKXKHHRVLDKIT 483

```



Qy 181 DTLHLMAKAGLTQQQHRLAQLLLILSHIRMSNKGMEHLYSMKCNVVPVLYDILLEM 240  
 Db 484 DTLHLMAKAGLTQQQHRLAQLLLILSHIRMSNKGMEHLYSMKCNVVPVLYDILLEM 543  
 Qy 241 LDAHRL 246  
 Db 544 LDAHRL 549  
 RESULT 4  
 US-09-041-886-35  
 ; Sequence 35, Application US/09041886  
 ; Patent No. 6235872  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bredesen, Dale E.  
 ; APPLICANT: Rabizadeh, Sharroz  
 ; TITLE OF INVENTION: Proapoptotic Peptides, Dependence  
 ; TITLE OF INVENTION: Polypeptides and Methods of Use  
 ; NUMBER OF SEQUENCES: 72  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Campbell & Flores LLP  
 ; STREET: 4370 La Jolla Village Drive, Suite 700  
 ; CITY: San Diego  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 92122  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/041.886  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Campbell, Cathryn A.  
 ; REGISTRATION NUMBER: 31,815  
 ; REFERENCE/DOCKET NUMBER: P-LJ 2626  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 535-9001  
 ; TELEFAX: (619) 535-8949  
 ; INFORMATION FOR SEQ ID NO: 35:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 595 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-041-886-35  
 Query Match 97.4%; Score 1197.5; DB 3; Length 595;  
 Best Local Similarity 95.9%; Pred. No. 3.6e-133;  
 Matches 236; Conservative 0; Mismatches 9; Indels 1; Gaps 1;  
 Qy 1 SLALSLTADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINAKRV 60  
 Db 305 SLALSLTADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINAKRV 364  
 Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGEMVEI 120  
 Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGEMVEI 424  
 Qy 121 FDMLLATSSFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXEKKDHHRVLDKIT 180  
 Db 425 FDMLLATSSFRMNLQGEFVCLKSIILLNSGVYTF-LSTLSKSEKDHHRVLDKIT 483  
 Qy 181 DTLHLMAKAGLTQQQHRLAQLLLILSHIRMSNKGMEHLYSMKCNVVPVLYDILLEM 240  
 Db 484 DTLHLMAKAGLTQQQHRLAQLLLILSHIRMSNKGMEHLYSMKCNVVPVLYDILLEM 543  
 Qy 241 LDAHRL 246  
 Db 544 LDAHRL 549

Db 544 LDAHRL 549  
 RESULT 5  
 US-08-453-998-2  
 ; Sequence 2, Application US/08453998  
 ; Patent No. 644438  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHAMBER, PIERRE  
 ; APPLICANT: METZGER, DANIEL  
 ; APPLICANT: WHITE, JOHN  
 ; TITLE OF INVENTION: METHOD FOR THE PREPARATION OF A PROTEIN  
 ; TITLE OF INVENTION: BY YEASTS USING AN INDUCIBLE SYSTEM, VECTORS AND  
 ; NUMBER OF SEQUENCES: 15  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN, DABBY & CUSHMAN  
 ; STREET: 1100 NEW YORK AVE., N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/453.998  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/161.064  
 ; FILING DATE: 03-DEC-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: CHAPIN, MARLANA K.  
 ; REGISTRATION NUMBER: 35,843  
 ; REFERENCE/DOCKET NUMBER: 1037/98493  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-861-3711  
 ; TELEFAX: 202-822-0944  
 ; TELEX: 6714627 CUSH  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 595 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-453-998-2  
 Query Match 97.4%; Score 1197.5; DB 4; Length 595;  
 Best Local Similarity 95.9%; Pred. No. 3.6e-133;  
 Matches 236; Conservative 0; Mismatches 9; Indels 1; Gaps 1;  
 Qy 1 SLALSLTADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINAKRV 60  
 Db 305 SLALSLTADQVMSALLDAEPPIYSEYDTPRPFSEASMMGLLTNLADRELVHMINAKRV 364  
 Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGEMVEI 120  
 Db 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRQKCVGEMVEI 424  
 Qy 121 FDMLLATSSFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXEKKDHHRVLDKIT 180  
 Db 425 FDMLLATSSFRMNLQGEFVCLKSIILLNSGVYTF-LSTLSKSEKDHHRVLDKIT 483  
 Qy 181 DTLHLMAKAGLTQQQHRLAQLLLILSHIRMSNKGMEHLYSMKCNVVPVLYDILLEM 240  
 Db 484 DTLHLMAKAGLTQQQHRLAQLLLILSHIRMSNKGMEHLYSMKCNVVPVLYDILLEM 543  
 Qy 241 LDAHRL 246  
 Db 544 LDAHRL 549

Db 544 LDAHRL 549

RESULT 6  
US-08-693-940-3  
; Sequence 3, Application US/08693940  
; Patent No. 6133027  
; GENERAL INFORMATION:  
; APPLICANT: Yee, Jiing-Kuan  
; APPLICANT: Friedman, Theodore  
; APPLICANT: Chen, Shin-Tai  
; TITLE OF INVENTION: Inducible Expression System  
; TITLE OF INVENTION: Useful in the Generation of Packaging Cell Lines for  
; TITLE OF INVENTION: Pseudotyped Retroviral Vectors  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bozicevic & Reed, LLP  
; STREET: 285 Hamilton Ave, Suite 200  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Fast-SEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/693,940  
; FILING DATE: 07-AUG-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Francis, Carol L  
; REGISTRATION NUMBER: 36,513  
; REFERENCE/DOCKET NUMBER: 6510-055001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-327-3400  
; TELEFAX: 650-327-3231  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 651 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-693-940-3

Query Match 97.4%; Score 1197.5; DB 3; Length 651;  
Best Local Similarity 95.9%; Pred. No. 4.1e-133;  
Matches 236; Conservative 0; Mismatches 9; Indels 1; Gaps 1

QY 1 SLALSIATADQWVSALLDAEPPLIYSEYDPTPFSEASMMGLLTNLADRELVHMINWAKEV 60  
Db 361 SLALSUTADQWVSALLDAEPPLIYSEYDPTPFSEASMMGLLTNLADRELVHMINWAKEV 420  
QY 61 PGFVDLTLDQVHLLECWLAILMIGLVWRSMEHPGKLLFAPNLLLDNRNGKCVGWEI 120  
Db 421 PGFVDLTLDQVHLLECWLAILMIGLVWRSMEHPVKLLFAPNLLLDNRNGKCVGWEI 480  
QY 121 FQMLLATSSRFMMNLQGEFVCLKSGIILNSGVYTFXXXXXXXEEKXDHIRVLDKIT 180  
Db 481 FQMLLATSSRFMMNLQGEFVCLKSGIILNSGVYTF-LSSTLKSLFEKXDHIRVLDKIT 539  
QY 181 DTLIHLMAKAGITLQOQHORIAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEW 240  
Db 540 DTLIHLMAKAGITLQOQHORIAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEW 599  
QY 241 LDAHRL 246

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,264
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02088
; FILING DATE: 28-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 110 298.2
; FILING DATE: 28-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,980
; REFERENCE/DOCKET NUMBER: P564-5019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 773 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1-423)
; OTHER INFORMATION: /note= "FLP recombinase domain."
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (424-428)
; OTHER INFORMATION: /note= "Linker peptide."
; NAME/KEY: misc feature
; LOCATION: (429-773)
; OTHER INFORMATION: /note= "Estrogen binding domain."
; US-08-564-264-1

```

```

Query Match 97.4%; Score 1197.5; DB 3; Length 773;
Best Local Similarity 95.9%; Pred. No. 5.2e-133; Indels 1; Gaps 1;
Matches 236; Conservative 0; Mismatches 9;
Qy 1 SLALSLTADQVMSALLDAEPPILYSEYDTPRPFSSEASNMGLLTNLADRELVHMINKRV 60
Db 483 SLALSLTADQVMSALLDAEPPILYSEYDTPRPFSSEASNMGLLTNLADRELVHMINKRV 542
Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNCKVCVEGMVEI 120
Db 543 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNCKVCVEGMVEI 602
Qy 121 FDMLLATSSFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRLDKIT 180
Db 603 FDMLLATSSFRMNLQGEFVCLKSIILLNSGVYTF-LSTLKSLEKOHHRVLDKIT 661
Qy 181 DTLIHLMAGAGLTQQOQHRLAQLLLILSHIRHMSNKGMEHLYSMCKQNVVPLYDILLEM 240
Db 562 DTLIHLMAGAGLTQQOQHRLAQLLLILSHIRHMSNKGMEHLYSMCKQNVVPLYDILLEM 721
Qy 241 LDAHRL 246
Db 722 LDAHRL 727

```

```

RESULT 9
5223606-5
; Patent No. 5223606
; APPLICANT: BLAUDIN DE THE, HUGHES, MARCHIO, AGNES, TIOLLAIS,
; PIERRE, DEJEAN, ANNE
; TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED
; PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/07/134,130
; FILING DATE: 17-DEC-1987
; PRIOR APPLICATION DATA:
; SEQ ID NO: 5;
; LENGTH: 410
; 5223606-5
Query Match 95.9%; Score 1180; DB 6; Length 410;
Best Local Similarity 95.5%; Pred. No. 2.5e-131;
Matches 235; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
Qy 1 SLALSLTADQVMSALLDAEPPILYSEYDTPRPFSSEASNMGLLTNLADRELVHMINKRV 60
Db 121 SLALSLTADQVMSALLDAEPPILYSEYDTPRPFSSEASNMGLLTNLADRELVHMINKRV 179
Qy 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNCKVCVEGMVEI 120
Db 180 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNCKVCVEGMVEI 239
Qy 121 FDMLLATSSFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDHIHRLDKIT 180
Db 240 FDMLLATSSFRMNLQGEFVCLKSIILLNSGVYTF-LSTLKSLEKOHHRVLDKIT 298
Qy 181 DTLIHLMAGAGLTQQOQHRLAQLLLILSHIRHMSNKGMEHLYSMCKQNVVPLYDILLEM 240
Db 299 DTLIHLMAGAGLTQQOQHRLAQLLLILSHIRHMSNKGMEHLYSMCKQNVVPLYDILLEM 358
Qy 241 LDAHRL 246
Db 359 LDAHRL 364

```

```

RESULT 10
US-08-836-620A-16
; Sequence 16, Application US/08836620A
; Patent No. 5958710
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Orphan receptor
; NUMBER OF SEQUENCES: 19
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA: US/08/836,620A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/03933
; FILING DATE:
; APPLICATION NUMBER: GB 9518272.1
; FILING DATE: 08-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9605550.4
; FILING DATE: 15-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9607532.0
; FILING DATE: 11-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9609576.5
; FILING DATE: 08-MAY-1996
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 596 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Rattus rattus
; US-08-836-620A-16
Query Match 94.9%; Score 1167.5; DB 2; Length 596;
Best Local Similarity 92.7%; Pred. No. 1.3e-129;

```

Matches 228; Conservative 5; Mismatches 12; Indels 1; Gaps 1;  
QY 1 SLALSTADQMSALLDAEPPILYSEYDTPRPSEASMMGLLTNLADRELVMINWAKRV 60  
DB 310 SPALSLTADQMSALLDAEPPILYSEYDTPRPSEASMMGLLTNLADRELVMINWAKRV 369  
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCEGMEVEI 120  
DB 370 PGFGDLNLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCEGMEVEI 429  
QY 121 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF-LSSSTUKSLEEKDHIHRVLDKIT 180  
DB 430 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF-LSSSTUKSLEEKDHIHRVLDKIN 488  
QY 181 DTLIHLMKAGLTLOQHOHRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPYDILLLEM 240  
DB 489 DTLIHLMKAGLTLOQHOHRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPYDILLLEM 548  
QY 241 LDAHRL 246  
DB 549 LDAHRL 554

RESULT 11  
US-09-660-979-1  
; Sequence 1, Application US/09660979  
; Patent No. 6500629  
; GENERAL INFORMATION:  
; APPLICANT: Cleaver, Brian  
; TITLE OF INVENTION: Materials and Methods for Detection and Quantitation of an Analyte  
; FILE REFERENCE: ELI-101XC1  
; CURRENT APPLICATION NUMBER: US/09/660, 979  
; PRIOR FILING DATE: 2000-09-13  
; PRIOR APPLICATION NUMBER: 60/153,627  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 264  
; TYPE: PRT  
; ORGANISM: Equus  
US-09-660-979-1

Query Match 93.2%; Score 1146; DB 4; Length 264;  
Best Local Similarity 91.5%; Pred. No. 1.4e-127;  
Matches 225; Conservative 7; Mismatches 12; Indels 2; Gaps 2;  
QY 1 SLALSTADQMSALLDAEPPILYSEYDTPRPSEASMMGLLTNLADRELVMINWAKRV 60  
DB 5 SPVLSLTAEQMISALLDAEPPVLYSYDTRPNEASMMGLLTNLADRELVMINWAKRV 64  
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCEGMEVEI 120  
DB 65 PGFVDLSLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCEGMEVEI 124  
QY 121 FDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTFXXXXXXEEDKHHRVLDKIT 180  
DB 125 FDMLLATSSRLRMMNLQGEFVCLKSIILLNSGVYTF-LSSSTUKSLEEKDHIHRVLDKMT 183  
QY 181 DTLIHLMKAGLTLOQHOHRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPYDILLLEM 240  
DB 184 DTLIHLMKAGLTLOQHOHRLAQLLLILSHIRMSNKGMEHLYSMCKKNVVPYDILLLEM 242  
QY 241 LDAHRL 246  
DB 243 LDAHRL 248

RESULT 12  
US-08-836-620A-10  
; Sequence 10, Application US/08836620A  
; Patent No. 5958710

GENERAL INFORMATION:  
; APPLICANT: Orphan receptor  
; TITLE OF INVENTION: Orphan receptor  
; NUMBER OF SEQUENCES: 19  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION NUMBER: US/08/836,620A  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP96/03933  
; FILING DATE:  
; APPLICATION NUMBER: GB 9518272.1  
; FILING DATE: 08-SEP-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9605550.4  
; FILING DATE: 15-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9607532.0  
; FILING DATE: 11-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9609576.5  
; FILING DATE: 08-MAY-1996  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 243 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-08-836-620A-10  
Query Match 78.2%; Score 961.5; DB 2; Length 243;  
Best Local Similarity 94.9%; Pred. No. 1e-105;  
Matches 188; Conservative 0; Mismatches 9; Indels 1; Gaps 1;  
QY 49 ELVHMNINWAKRVPGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDR 108  
DB 1 ELVHMNINWAKRVPGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPVXLLFAPNLLDR 60  
QY 109 NOGKCEGMEVEIFDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTFXXXXXXE 168  
DB 61 NOGKCEGMEVEIFDMLLATSSRFMMNLQGEFVCLKSIILLNSGVYTF-LSSSTUKSLEE 119  
QY 169 KDHIHRVLDKITDTLIHLMKAGLTLOQHOHRLAQLLLILSHIRMSNKGMEHLYSMCK 228  
DB 120 KDHIHRVLDKITDTLIHLMKAGLTLOQHOHRLAQLLLILSHIRMSNKGMEHLYSMCK 179  
QY 229 NVVPLYDILLLEMLDAHRL 246  
DB 180 NVVPLYDILLLEMLDAHRL 197  
RESULT 13  
US-08-836-620A-9  
; Sequence 9, Application US/08836620A  
; Patent No. 5958710  
; GENERAL INFORMATION:  
; APPLICANT: Orphan receptor  
; TITLE OF INVENTION: Orphan receptor  
; NUMBER OF SEQUENCES: 19  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION NUMBER: US/08/836,620A  
; FILING DATE:  
; PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: PCT/EP96/03933
; FILING DATE:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; US-836-620A-9

Query Match          77.4%; Score 951.5; DB 2; Length 243;
Best Local Similarity 93.4%; Pred. No. 1.5e-104;
Matches 185; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

QY 49 ELVHMINWAKRVGFDLTLDHDOVHLLCAWLEITMIGLVWRSMEHPGKLLFAPNLLDR 108
DB 1 ELVHMINWAKRVGFDLNDHDOVHLLCAWLEITMIGLVWRSMEHPGKLLFAPNLLDR 60

QY 109 NOGKCEGVMEIFDMLLATSSFRMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEE 168
DB 61 NOGKCEGVMEIFDMLLATSSFRMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEE 119

QY 169 KDHHRVLDKITDTLHLMKAGLTLOOQHORLAQLLLILSHIRHMSNKGMEHLYSNKCK 228
DB 120 KDHHRVLDKITDTLHLMKAGLTLOOQHORLAQLLLILSHIRHMSNKGMEHLYSNKCK 179

QY 229 NVVPLYDLLLEMLDAHRL 246
DB 180 NVVPLYDLLLEMLDAHRL 197

RESULT 14
US-08-836-620A-8
; Sequence 8, Application US/08836620A
; Patent No. 5958710
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Orphan receptor
; NUMBER OF SEQUENCES: 19
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836, 620A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/03933
; FILING DATE:
; APPLICATION NUMBER: GB 9518272.1
; FILING DATE: 08-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9605550.4
; FILING DATE: 15-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9607532.0
; FILING DATE: 11-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9609576.5
; FILING DATE: 08-MAY-1996
```

```
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Rattus rattus
; US-08-836-620A-8
```

```
Query Match          77.0%; Score 946.5; DB 2; Length 243;
Best Local Similarity 92.9%; Pred. No. 6e-104;
Matches 184; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY 49 ELVHMINWAKRVGFDLTLDHDOVHLLCAWLEITMIGLVWRSMEHPGKLLFAPNLLDR 108
DB 1 ELVHMINWAKRVGFDLNDHDOVHLLCAWLEITMIGLVWRSMEHPGKLLFAPNLLDR 60

QY 109 NOGKCEGVMEIFDMLLATSSFRMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEE 168
DB 61 NOGKCEGVMEIFDMLLATSSFRMMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEE 119

QY 169 KDHHRVLDKITDTLHLMKAGLTLOOQHORLAQLLLILSHIRHMSNKGMEHLYSNKCK 228
DB 120 KDHHRVLDKITDTLHLMKAGLTLOOQHORLAQLLLILSHIRHMSNKGMEHLYSNKCK 179

QY 229 NVVPLYDLLLEMLDAHRL 246
DB 180 NVVPLYDLLLEMLDAHRL 197
```

```
RESULT 15
US-09-893-666A-2
; Sequence 2, Application US/09893666A
; Patent No. 6759568
; GENERAL INFORMATION:
; APPLICANT: YAMASHITA, ICHIRO
; TITLE OF INVENTION: High estrogen-sensitive medaka fish
; FILE REFERENCES: 210217US-620-7249-0
; CURRENT APPLICATION NUMBER: US/09/893, 666A
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: JP 2000-247729
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 575
; ORGANISM: Oryzias latipes
; US-09-893-666A-2
```

```
Query Match          64.4%; Score 792.5; DB 4; Length 575;
Best Local Similarity 63.0%; Pred. No. 3.9e-85;
Matches 155; Conservative 39; Mismatches 43; Indels 9; Gaps 2;

QY 5 SUTADQWVSALLDAEPPILYSEYDPTPRPFSEASMMGLTNLADRELVHMINWAKRVPGFV 64
DB 268 SIPPEQVLLQLQGAEPPIILCSRQKLSRPTVETVMTLLTSMADKELVHMINWAKKLPGL 327

QY 65 DLTLDQVHLLCAWLEITMIGLVWRSMEHPGKLLFAPNLLDRNOGKCEGVMEIFDML 124
DB 328 QLSLHDQVLLLESSWLEVMIGLWRSIHCPGKLIFAQDILDRNEGDCVEGMEIFDML 387

QY 125 LATSSFRMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDH-----IHRVLDKIT 180
DB 388 LATASRFRVLKLPKEEFVCLKAIILLNSGAFSFCGTGTM-----EPLHNSAASQSMIDTIT 442

QY 181 DTLHLMKAGLTLOOQHORLAQLLLILSHIRHMSNKGMEHLYSNKCKNVVPLYDLLLEML 240
DB 443 DALIHYISQGYLAQEARRQAQLLLILSHIRHMSNKGMEHLYSNKCKNVVPLYDLLLEML 502

QY 241 LDAHRL 246
DB 503 LDAHRL 508
```

Search completed: November 8, 2004, 08:29:28  
Job time : 15.5592 secs



CC lung, breast, lymphoid, gastrointestinal, genito-urinary tract  
 CC adenocarcinomas and other malignancies such as colon cancers, renal- cell  
 CC carcinoma, prostate cancer, non-small cell carcinoma of the lung, cancer  
 CC of the small intestine and cancer of the oesophagus. The invention is  
 CC useful for constructing selective molecular gene switches for regulating  
 CC gene function in plants and transgenic animals. It is also useful in gene  
 CC therapy. The present sequence is human ER alpha LBD -zinc finger array  
 CC (C7) fusion protein  
 XX  
 SQ Sequence 414 AA;

Query Match 98.1%; Score 1206.5; DB 6; Length 414;  
 Best Local Similarity 96.3%; Pred. No. 2.1e-134;  
 Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
 QY 1 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
 DB 122 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 181  
 QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVGMEI 120  
 DB 182 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVGMEI 241  
 QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXEEDKHHRVLDKIT 180  
 DB 242 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 300  
 QY 181 DTLIHLMKAGLTLOQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM 240  
 DB 301 DTLIHLMKAGLTLOQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM 360  
 QY 241 LDAHRL 246  
 DB 361 LDAHRL 366

RESULT 2  
 AAB61498  
 ID AAB61498 standard; protein; 422 AA.  
 XX  
 AC AAB61498;  
 XX  
 DT 04-APR-2001 (first entry)  
 XX  
 DE Protein encoded by human estrogen receptor alpha isoform #1.  
 XX  
 KW Human; estrogen receptor alpha; cancer; osteoporosis; bone; Alzheimer's;  
 KW Cardiovascular.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200100823-A1.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 27-JUN-2000; 2000WO-EP005981.  
 XX  
 PR 29-JUN-1999; 99IT-MI001433.  
 XX  
 PA (EUMO-) EURO MOLECULAR BIOLOGY LAB.  
 XX  
 PI Cannon F, Dengler S, Flouriot G;  
 XX  
 DR WPI; 2001-137955/14.  
 XX  
 PT Novel isoforms of human estrogen receptor alpha useful for preparing  
 PT therapeutic agents for treating cancer, osteoporosis, Alzheimer's disease  
 PT and cardiovascular diseases.  
 XX  
 PS Claim 4; Page 45-46; 53pp; English.  
 XX  
 CC The present invention relates to a human estrogen receptor (HER)-alpha  
 CC isoform. Molecules which modulate the activity of the estrogen receptor

CC are useful for the preparation of therapeutic agents for treating cancer,  
 CC osteoporosis and other bone disorders, Alzheimer's disease and  
 CC cardiovascular diseases  
 XX  
 SQ Sequence 422 AA;

Query Match 98.1%; Score 1206.5; DB 4; Length 422;  
 Best Local Similarity 96.3%; Pred. No. 2.2e-134;  
 Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
 QY 1 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
 DB 132 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 191  
 QY 61 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVGMEI 120  
 DB 192 PGFVDLTLDQVHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVGMEI 251  
 QY 121 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXEEDKHHRVLDKIT 180  
 DB 252 FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 310  
 QY 181 DTLIHLMKAGLTLOQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM 240  
 DB 311 DTLIHLMKAGLTLOQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM 370  
 QY 241 LDAHRL 246  
 DB 371 LDAHRL 376

RESULT 3  
 AAE35276  
 ID AAE35276 standard; protein; 438 AA.  
 XX  
 AC AAE35276;  
 XX  
 DT 28-MAY-2003 (first entry)  
 XX  
 DE C7LBD8S fusion (wild-type) protein.  
 XX  
 KW Oestrogen receptor; ER alpha; ligand binding domain; genetic disease;  
 KW acquired disease; cell proliferative disorder; cancer; adenocarcinoma;  
 KW LBD; gene switch; transgenic animal; transgenic; gene therapy; human;  
 KW zinc finger array; C7; fusion protein.  
 XX  
 OS Homo sapiens.  
 OS Unidentified.  
 OS Chimeric.  
 XX  
 PN WO200297050-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 31-MAY-2002; 2002WO-US016946.  
 XX  
 PR 31-MAY-2001; 2001US-0294839P.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 XX  
 PI Bracken KR, De Los Angeles JE, Huang Y, Kadan MJ, Ksander GM;  
 PI Zerby DB;  
 XX  
 DR WPI; 2003-156794/15.  
 DR N-PSDB; AAD53876.  
 XX  
 PT New mutant estrogen receptor ligand binding domain capable of interacting  
 PT with non-endogenous ligand, useful e.g. in combination with a ligand for  
 PT constructing selective molecular gene switches for regulating gene  
 PT function.  
 XX  
 PS Example 4; Page 120-122; 159pp; English.  
 XX



CC The invention relates to a mutant oestrogen receptor (ER) alpha-ligand  
 CC binding domain (LBD) which comprises an amino acid modification in region  
 CC 1, region 2 or both and interacting with a non-endogenous ligand as a  
 CC result of the amino acid modification. Sequences of the invention are  
 CC useful for treatment of genetic diseases, acquired diseases and any other  
 CC conditions including cell proliferative disorders such as cancer e.g.  
 CC lung, breast, lymphoid, gastrointestinal, genito-urinary tract  
 CC adenocarcinomas and other malignancies such as colon cancers, renal- cell  
 CC carcinoma, prostate cancer, non-small cell carcinoma of the lung, cancer  
 CC of the small intestine and cancer of the oesophagus. The invention is  
 CC useful for constructing selective molecular gene switches for regulating  
 CC gene function in plants and transgenic animals. It is also useful in gene  
 CC therapy. The present sequence is human ER alpha LBD -zinc finger array  
 CC (C7) fusion protein  
 XX  
 XX SQ Sequence 438 AA;

Query Match 98.1%; Score 1206.5; DB 6; Length 438;  
 Best Local Similarity 96.3%; Pred. No. 2.3e-134;  
 Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
 QY 1 SLALSUTADQVMSALLDAEPPIYSEYDTPRPSEASMGILLTNLADRELVHMINWAKRV 60  
 DB 146 SLALSUTADQVMSALLDAEPPIYSEYDTPRPSEASMGILLTNLADRELVHMINWAKRV 205  
 QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVRSMEHPGKLLFAPNLLDRNOGKCVGMEVEI 120  
 DB 206 PGFVDLTLDQVHLLCAWLEILMIGLVRSMEHPGKLLFAPNLLDRNOGKCVGMEVEI 265  
 QY 121 FDMLLATSSFRMNLQGEFVCLKSIILLNSGYTTFXXXXXXXBEKDHHRVLDKIT 180  
 DB 266 FDMLLATSSFRMNLQGEFVCLKSIILLNSGYTTF-LSSLTKSLEEKDHHRVLDKIT 324  
 QY 181 DTLHLMAKAGLTQQOQHRLAQLLLSHIRHMSKMGMEHLYSMCKKNVVPVLDLLE 240  
 DB 325 DTLHLMAKAGLTQQOQHRLAQLLLSHIRHMSKMGMEHLYSMCKKNVVPVLDLLE 384  
 QY 241 LDAHRL 246  
 DB 385 LDAHRL 390

RESULT 4  
 AAB61499  
 ID AAB61499 standard; protein; 457 AA.  
 XX  
 XX AC AAB61499;  
 XX  
 XX 04-APR-2001 (first entry)  
 XX Protein encoded by human estrogen receptor alpha isoform #2.  
 XX  
 XX Human; estrogen receptor alpha; cancer; osteoporosis; bone; Alzheimer's;  
 XX cardiovascular.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200100823-A1.  
 XX  
 XX 04-JAN-2001.  
 XX  
 XX 27-JUN-2000; 2000WO-EP005981.  
 XX  
 XX 29-JUN-1999; 99IT-MI001433.  
 XX (EUMO-) EURO MOLECULAR BIOLOGY LAB.  
 XX Gannon F, Denger S, Flouriot G;  
 XX WPI; 2001-137955/14.  
 XX  
 XX Novel isoforms of human estrogen receptor alpha useful for preparing  
 XX therapeutic agents for treating cancer, osteoporosis, Alzheimer's disease  
 PT

PT and cardiovascular diseases.  
 XX Claim 4; Page 46-48; 53pp; English.  
 XX  
 XX The present invention relates to a human estrogen receptor (hER)-alpha  
 XX isoform. Molecules which modulate the activity of the estrogen receptor  
 XX are useful for the preparation of therapeutic agents for treating cancer,  
 XX osteoporosis and other bone disorders, Alzheimer's disease and  
 XX cardiovascular diseases  
 XX  
 XX SQ Sequence 457 AA;

Query Match 98.1%; Score 1206.5; DB 4; Length 457;  
 Best Local Similarity 96.3%; Pred. No. 2.4e-134;  
 Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
 QY 1 SLALSUTADQVMSALLDAEPPIYSEYDTPRPSEASMGILLTNLADRELVHMINWAKRV 60  
 DB 167 SLALSUTADQVMSALLDAEPPIYSEYDTPRPSEASMGILLTNLADRELVHMINWAKRV 226  
 QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVRSMEHPGKLLFAPNLLDRNOGKCVGMEVEI 120  
 DB 227 PGFVDLTLDQVHLLCAWLEILMIGLVRSMEHPGKLLFAPNLLDRNOGKCVGMEVEI 286  
 QY 121 FDMLLATSSFRMNLQGEFVCLKSIILLNSGYTTFXXXXXXXBEKDHHRVLDKIT 180  
 DB 287 FDMLLATSSFRMNLQGEFVCLKSIILLNSGYTTF-LSSLTKSLEEKDHHRVLDKIT 345  
 QY 181 DTLHLMAKAGLTQQOQHRLAQLLLSHIRHMSKMGMEHLYSMCKKNVVPVLDLLE 240  
 DB 346 DTLHLMAKAGLTQQOQHRLAQLLLSHIRHMSKMGMEHLYSMCKKNVVPVLDLLE 405  
 QY 241 LDAHRL 246  
 DB 406 LDAHRL 411

RESULT 5  
 AAB36684  
 ID AAB36684 standard; protein; 480 AA.  
 XX  
 XX AC AAB36684;  
 XX  
 XX 15-MAR-2001 (first entry)  
 XX Mammalian two-hybrid protein SEQ ID NO:8.  
 XX  
 XX Mammalian; two-hybrid assay; hybrid protein; hybrid gene; detection;  
 XX reporter gene; DNA-binding region; transcriptional activation;  
 XX fused protein; protein interaction.  
 XX  
 XX Mammalia.  
 XX Synthetic.  
 XX  
 XX WO2000071743-A1.  
 XX  
 XX 30-NOV-2000.  
 XX  
 XX 25-MAY-2000; 2000WO-JP003353.  
 XX  
 XX 25-MAY-1999; 99JP-00144946.  
 XX (EISA ) EISAI CO LTD.  
 XX Teukahara K, Hida T, Nakamura K, Yoshitomi H;  
 XX WPI; 2001-025169/03.  
 XX N-PSDB; AAC88199.  
 XX  
 XX Novel two hybrid detection method comprising fusing two proteins with a  
 XX DNA binding sequence and a transcription activation sequence respectively  
 XX for detecting interaction of the proteins in mammalian cells.  
 XX

PS Example 2; Page 35-37; 63pp; Japanese.

XX The present invention describes a method for detecting the interaction of  
CC a first and a second protein within a mammalian cell. The method  
CC comprises a fusion protein of the first protein with two or more  
CC transcription activation sequences (which may be the same or different),  
CC and a fusion protein of the second protein with a DNA-binding sequence.  
CC These are expressed in a mammalian cell containing DNA carrying a  
CC reporter gene downstream of a sequence binding to the DNA-binding  
CC sequence; and the expression of the reporter gene is detected to indicate  
CC interaction of the two proteins. The method is useful for the  
CC identification and examination of protein interactions within the  
CC mammalian cell, and screening of potential drugs targeting them. The  
CC present sequence represents a hybrid protein from an example given in the  
XX present invention

XX Sequence 480 AA;

SQ Query Match 98.1%; Score 1206.5; DB 4; Length 480;  
Best Local Similarity 96.3%; Pred. No. 2.6e-134; Indels 1; Gaps 1;  
Matches 237; Conservative 0; Mismatches 8;

QY 1 SLALSITADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 174 SLALSITADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 233  
QY 61 PGFVDLTLDQVHLLCAWLEILMGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEVEI 120  
DB 234 PGFVDLTLDQVHLLCAWLEILMGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEVEI 293  
QY 121 FDMLLATSRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDTHRVLDKIT 180  
DB 294 FDMLLATSRFRMNLQGEFVCLKSIILLNSGVYTF-LSSSTLKSLEEKDTHRVLDKIT 352  
QY 181 DTLIHLMAKAGLTLOOQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEM 240  
DB 353 DTLIHLMAKAGLTLOOQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEM 412  
QY 241 LDAHRL 246  
DB 413 LDAHRL 418

RESULT 6

AAAY21626  
ID AAY21626 standard; protein; 595 AA.

XX AC AAY21626;

DT 1-AUG-1999 (first entry)

DE DE Ligand binding domain of nuclear receptor hER.

XX Thyroid hormone receptor; aromatic compound; ligand binding domain;  
KW alpha-glycerophosphate dehydrogenase; cardiac; obesity; triglyceride;  
KW plasma cholesterol; anti-hypertriglyceridaemic; atherosclerosis; GPDH;  
KW thyroid hormone replacement therapy; nuclear receptor.

XX OS Homo sapiens.

XX PN WO9926966-A2.

XX PD 03-JUN-1999.

XX PF 25-NOV-1998; 98WO-US025296.

XX PR 26-NOV-1997; 97US-00980115.

XX PA (REGC ) UNIV CALIFORNIA.

XX Scanlan TS, Baxter JD, Fletcher RJ, Wagner RL, Kushner PJ;  
PI Aprilletti JW, West BL, Shiao AK;

XX

DR WPI; 1999-357810/30.

XX Modulating activity of a thyroid hormone receptor.

XX Disclosure; Fig 3G-R; 447pp; English.

XX The invention relates to a method for modulating activity of a thyroid  
CC hormone receptor that comprises administration of an aromatic compound  
CC which fits spatially and preferentially into a thyroid hormone ligand  
CC binding domain. The aromatic compound (of a specified formula) can be  
CC used to increase alpha-glycerophosphate dehydrogenase (GPDH) levels, at  
CC levels which do not significantly modify cardiac GPDH levels and are  
CC indicated in the treatment of obesity. The compound also lower total  
CC plasma cholesterol and triglyceride levels and can be used as anti-  
CC hypertriglyceridaemic agents. The compound may also be used for treating  
CC atherosclerosis and may be indicated in thyroid hormone replacement  
CC therapy in patients with compromised cardiac function. Sequences AAY21621  
CC - 636 amino acid sequences of ligand binding domains of several members  
CC of the nuclear receptor superfamily

XX Sequence 595 AA;

SQ Query Match 98.1%; Score 1206.5; DB 2; Length 595;  
Best Local Similarity 96.3%; Pred. No. 3.5e-134;  
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 SLALSITADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 305 SLALSITADQMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364  
QY 61 PGFVDLTLDQVHLLCAWLEILMGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEVEI 120  
DB 365 PGFVDLTLDQVHLLCAWLEILMGLVWRSMEHPGKLLFAPNLLLDNRQKCVGMEVEI 424  
QY 121 FDMLLATSRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEEKDTHRVLDKIT 180  
DB 425 FDMLLATSRFRMNLQGEFVCLKSIILLNSGVYTF-LSSSTLKSLEEKDTHRVLDKIT 483  
QY 181 DTLIHLMAKAGLTLOOQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEM 240  
DB 484 DTLIHLMAKAGLTLOOQHQRQAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEM 543  
QY 241 LDAHRL 246  
DB 544 LDAHRL 549

RESULT 7

AAG84505

ID AAG84505 standard; protein; 595 AA.

XX AC AAG84505;

DT 10-SEP-2001 (first entry)

DE Human oestrogen receptor alpha protein.

XX Ligand dependent transcriptional factor; oestrogen receptor; ER;  
KW glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;  
KW MR; peroxisome proliferator-activated receptor protein; PPAR;  
KW progesterone receptor protein; PR; pregnane X receptor protein; PXR;  
KW thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;  
KW transactivation; ERalpha; breast cancer.

XX OS Homo sapiens.

XX PN WO200142307-A1.

XX PD 14-JUN-2001.

XX PF 01-DEC-2000; 2000WO-JP008553.

XX PR 07-DEC-1999; 99JP-00348022.

Human oestrogen receptor alpha protein mutant S578P.

Db	484	DTLIHLMAKAGITLQQQHQRQAQLLLSHIRHMSNKGMEHLYSMCKKNVVPDYDLLLEM	543
QY	241	LDAHRL 246	
Db	544	LDAHRL 549	
RESULT 9			
AA	84506		
ID	AAG84506	standard; protein; 595 AA.	
XX			
AC	AAG84506;		
XX			
DT	10-SEP-2001	(first entry)	
XX			
DE	Human oestrogen receptor alpha protein mutant K303R.		
XX			
KW	Ligand dependent transcriptional factor; oestrogen receptor; ER;		
KW	glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;		
KW	GR; peroxisome proliferator-activated receptor protein; PPAR;		
KW	progesterone receptor protein; PR; pregnane X receptor protein; PXR;		
KW	thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;		
XX	transactivation; ERalpha; breast cancer; mutant; mutein.		
OS	Homo sapiens.		
XX			
PN	WO200142307-A1.		
XX			
PD	14-JUN-2001.		
XX			
PF	01-DEC-2000; 2000WO-JP008553.		
XX			
PR	07-DEC-1999; 99JP-00348022.		
PR	27-DEC-1999; 99JP-00370667.		
PR	07-JUL-2000; 2000JP-00207011.		
PR	21-JUL-2000; 2000JP-00220508.		
PR	02-AUG-2000; 2000JP-00234053.		
PR	03-AUG-2000; 2000JP-00235460.		
PR	03-AUG-2000; 2000JP-00235461.		
PR	03-AUG-2000; 2000JP-00235463.		
XX	(SUMO ) SUMITOMO CHEM CO LTD.		
PA			
XX			
PI	Saito K, Ohe N, Satoh H;		
XX			
DR	WPI; 2001-367866/38.		
XX			
PS	Claim 15; Page 170-174; 276pp; English.		
XX			
CC	The present invention relates to ligand dependent transcriptional factors		
CC	including oestrogen receptor (ER) alpha and beta protein, glucocorticoid		
CC	receptor protein (GR), mineralocorticoid receptor protein (MR),		
CC	peroxisome proliferator-activated receptor protein (PPAR), progesterone		
CC	receptor protein (PR), pregnane X receptor protein (PXR), thyroid hormone		
CC	receptor protein (TR) and vitamin D receptor protein (VDR), the nucleic		
CC	acids encoding them and cells comprising them and a specified reporter		
CC	gene for the ligand dependent transcriptional factor. These proteins are		
CC	useful in the modulation of ligand dependent transcriptional factor		
CC	activity. The cells, mutant ERalpha and the polynucleotide encoding it		
CC	may be used in assays for qualitatively analysing an activity for		
CC	transactivation of a reporter gene by a test ERalpha, for screening		
CC	mutant ligand dependent transcriptional factors, for evaluating an		
CC	activity for transactivation of a reporter gene by a test ERalpha and/or		
CC	for screening a compound useful for treating a disorder of a mutant		
CC	ERalpha, especially breast cancer		
XX			
SQ	Sequence 595 AA;		
Query Match			
Best Local Similarity 98.1%; Score 1206.5; DB 4; Length 595;			
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;			
QY	1	SLALSLTADQMVSAALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV	60
Db	305	SLALSLTADQMVSAALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV	364
QY	61	PGFVDLTLDQVHLLLECAWLILMIGLVWRSMEHFGKLLFAPNLLIDRNOGKCVSGMVEI	120
Db	365	PGFVDLTLDQVHLLLECAWLILMIGLVWRSMEHFGKLLFAPNLLIDRNOGKCVSGMVEI	424
QY	121	FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVVTFXXXXXXEKKDHHRVLDKIT	180
Db	425	FDMLLATSSRRFRMNLQGEFVCLKSIILLNSGVVTF-LSSLKSLSEKDHHRVLDKIT	483
QY	181	DTLIHLMAKAGITLQQQHQRQAQLLLSHIRHMSNKGMEHLYSMCKKNVVPDYDLLLEM	240
Db	484	DTLIHLMAKAGITLQQQHQRQAQLLLSHIRHMSNKGMEHLYSMCKKNVVPDYDLLLEM	543
QY	241	LDAHRL 246	
Db	544	LDAHRL 549	
RESULT 10			
AB	76378		
ID	ABB76378	standard; protein; 595 AA.	
XX			
AC	ABB76378;		
XX			
DT	22-AUG-2002	(first entry)	
XX			
DE	Human nuclear oestrogen receptor alpha.		
XX			
KW	Oestrogen; receptor; human; transgenic mouse; cytostatic;		
KW	antiinflammatory; antidiabetic; endocrine; anorectic; hepatotropic.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Domain	180..262	
FT		/note= "DNA-binding domain"	
FT	Region	263..301	
FT		/note= "D hinge region"	
FT	Domain	302..552	
FT		/note= "ligand-binding domain"	
XX			
PN	WO200228175-A2.		
XX			
PD	11-APR-2002.		
XX			
PF	28-SEP-2001; 2001WO-IB002246.		
XX			
PR	03-OCT-2000; 2000PR-00012570.		
PR	11-MAY-2001; 2001US-00853033.		
XX			
PA	(ADER-) ADEREGEM ASSOC DEV RECH EN GENETIQ.		
XX			
PI	Chambon P, Metzger D;		
XX			
DR	WPI; 2002-463217/49.		
DR	N-PSDB; ABL57497.		
XX			
PT	A transgenic mouse, useful in screening for medicaments for the treatment		
PT	of e.g., diabetes or skin cancers, comprises a fusion protein between a		
PT	recombinase Cre, and a modified ligand binding domain of the nuclear		
PT	estrogen receptor alpha.		
XX			
PS	Claim 6; Page 131-132; 149pp; English.		
XX			
CC	The present sequence is the protein sequence of the human nuclear		
CC	oestrogen receptor alpha (1). The invention relates to a non-human		



XX ADO42788;  
AC 26-AUG-2004 (first entry)  
DT  
DE  
XX  
DE Wild type human oestrogen receptor-alpha (ER) protein.  
XX  
KW human; oestrogen receptor-alpha; ER; ER activity regulator substance;  
KW anti-oestrogen substance.  
XX  
OS Homo sapiens.  
XX WO2004046352-A1.  
PN  
XX  
PD 03-JUN-2004.  
XX  
XX 14-NOV-2003; 2003WO-JP014494.  
PF  
XX 15-NOV-2002; 2002JP-00331994.  
PR  
XX 15-NOV-2002; 2002JP-00331995.  
PR  
XX 15-NOV-2002; 2002JP-00331996.  
PR  
XX (SUMO ) SUMITOMO CHEM CO LTD.  
PA  
XX Fujimori K;  
PI  
XX  
PI WPI; 2004-431978/40.  
DR  
XX  
XX New mutant estrogen receptor-alpha useful for determining effectiveness  
PT of treatment by estrogen receptor activity regulator substance and  
PT antiestrogen substance.  
PT  
XX  
PS Claim 1; SEQ ID NO 1; 111pp; Japanese.  
XX  
XX The invention comprises the amino acid sequences of mutant human  
CC oestrogen receptor-alpha (ER) proteins. The mutant ER proteins of the  
CC invention are useful for determining the effectiveness of a treatment by  
CC an ER activity regulator substance, and for determining the effectiveness  
CC of a treatment by an anti-oestrogen substance. The present amino acid  
CC sequence represents the wild-type human ER protein.  
XX  
SQ Sequence 595 AA;  
Query Match 98.1%; Score 1206.5; DB 8; Length 595;  
Best Local Similarity 96.3%; Pred. No. 3.5e-134;  
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
QY 1 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 305 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364  
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMVEI 120  
DB 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMVEI 424  
QY 121 FDMLLATSRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXEEXKHHRVLDKIT 180  
DB 425 FDMLLATSRFRMNLQGEFVCLKSIILLNSGVYTF-LSSSTLKSLEEKDHIHRVLDKIT 483  
QY 181 DTLIHLMKAGLTLOOQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPYDILLLEM 240  
DB 484 DTLIHLMKAGLTLOOQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPYDILLLEM 543  
QY 241 LDAHRL 246  
DB 544 LDAHRL 549  
RESULT 13  
ADO42830  
ID ADO42830 standard; protein; 595 AA.  
XX  
XX ADO42830;  
AC

XX 26-AUG-2004 (first entry)  
DT  
DE Human oestrogen receptor-alpha (ER) protein.  
XX  
KW human; oestrogen receptor-alpha; ER; ER activity regulator substance;  
KW anti-oestrogen substance.  
XX  
OS Homo sapiens.  
XX WO2004046352-A1.  
PN  
XX  
PD 03-JUN-2004.  
XX  
XX 14-NOV-2003; 2003WO-JP014494.  
PF  
XX 15-NOV-2002; 2002JP-00331994.  
PR  
XX 15-NOV-2002; 2002JP-00331995.  
PR  
XX 15-NOV-2002; 2002JP-00331996.  
PR  
XX (SUMO ) SUMITOMO CHEM CO LTD.  
PA  
XX Fujimori K;  
PI  
XX  
PI WPI; 2004-431978/40.  
DR  
XX  
XX New mutant estrogen receptor-alpha useful for determining effectiveness  
PT of treatment by estrogen receptor activity regulator substance and  
PT antiestrogen substance.  
PT  
XX  
PS Disclosure; Fig 19; 111pp; Japanese.  
XX  
XX The invention comprises the amino acid sequences of mutant human  
CC oestrogen receptor-alpha (ER) proteins. The mutant ER proteins of the  
CC invention are useful for determining the effectiveness of a treatment by  
CC an ER activity regulator substance, and for determining the effectiveness  
CC of a treatment by an anti-oestrogen substance. The present amino acid  
CC sequence represents a human ER protein.  
XX  
SQ Sequence 595 AA;  
Query Match 98.1%; Score 1206.5; DB 8; Length 595;  
Best Local Similarity 96.3%; Pred. No. 3.5e-134;  
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
QY 1 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 60  
DB 305 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADRELVHMINWAKRV 364  
QY 61 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMVEI 120  
DB 365 PGFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQKCVGMVEI 424  
QY 121 FDMLLATSRFRMNLQGEFVCLKSIILLNSGVYTFXXXXXXEEXKHHRVLDKIT 180  
DB 425 FDMLLATSRFRMNLQGEFVCLKSIILLNSGVYTF-LSSSTLKSLEEKDHIHRVLDKIT 483  
QY 181 DTLIHLMKAGLTLOOQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPYDILLLEM 240  
DB 484 DTLIHLMKAGLTLOOQHQRQAQLLLILSHIRHMSNKGMEHLYSMCKKNVVPYDILLLEM 543  
QY 241 LDAHRL 246  
DB 544 LDAHRL 549  
RESULT 14  
AAB26784  
ID AAB26784 standard; protein; 244 AA.  
XX  
XX AAB26784;  
XX  
DT 18-JAN-2001 (first entry)

Oestrogen receptor protein sequence.

Homology model; ligand binding domain; glucocorticoid receptor; AIDS; hypertension; diabetes; obesity; glaucoma; depression; wound; human; protein co-ordinate data; thyroid hormone receptor; oestrogen receptor. Unidentified.

WO200052050-A2.

08-SEP-2000.

01-MAR-2000; 2000WO-GB000727.

01-MAR-1999; 99GB-00004441.

22-APR-1999; 99GB-00009151.

(KARO-) KARO BIO AB.

Gillner M, Greenidge P; WPI; 2000-549565/50.

Designing a homology model of the ligand binding domain of a glucocorticoid receptor displayed as a three-dimensional image, useful for identifying agonists and antagonists for treating e.g. inflammation, hypertension, glaucoma, diabetes.

Disclosure; Fig 6; 246pp; English.

This invention relates to a method for designing an homology model of the ligand binding domain of a glucocorticoid receptor. The homology model may be displayed as a three-dimensional image. The method comprises: (a) providing an amino acid sequence and an x-ray crystallographic structure of the ligand binding domain of a thyroid, oestrogen or progesterone receptor; (b) modifying the x-ray crystallographic structure to take account of differences between the amino acid configuration of the ligand binding domain of the glucocorticoid receptor and the thyroid, oestrogen, or progesterone receptor; (c) verifying the accuracy of the homology model by comparing it with experimentally-determined binding properties of a number of ligands for the glucocorticoid receptor; and (d) modifying the homology model for greater consistency with the binding properties. The homology model is useful for drug screening and designing ligands (agonists and antagonists) capable of binding to a glucocorticoid receptor. The identified agonists are useful for the treatment of inflammation and also in immunosuppressive therapy. The identified antagonists are useful for the treatment of hypertension, diabetes, obesity, glaucoma, depression, acquired immune deficiency syndrome (AIDS) and wounds. The homology models are also useful for electronic screening of compound databases, de novo drug design and/or prediction of binding affinities of glucocorticoid receptor ligands for the receptor by

Query Match 97.8%; Score 1202.5; DB 3; Length 244; Best Local Similarity 96.3%; Pred. No. 3e-134; Matches 236; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

1 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADELVHMINAKRV 60  
|||||

1 SLALSITADQVMSALLDAEPPILYSEYDTPRPFSEASMMGLLTNLADELVHMINAKRV 60  
|||||

61 PGFVDLTLDQVHLLCAEILMIGLVWRSMEHPGKLLPAPNLLDRNQKCVGWEI 120  
|||||

61 PGFVDLTLDQVHLLCAEILMIGLVWRSMEHPGKLLPAPNLLDRNQKCVGWEI 120  
|||||

QY 121 FDMLLATSSFRMMNLQGEFVCLKSIILLNSGVYTFXXXXXXXEKDHIHRVLDKIT 180  
|||||

DB 121 FDMLLATSSFRMMNLQGEFVCLKSIILLNSGVYTF-LSSTLSLEKDIHRVLDKIT 179  
|||||

QY 181 DTILHMAKAGLTQQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLVYDLLLEM 240  
|||||

DB 180 DTILHMAKAGLTQQOQHRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLVYDLLLEM 239  
|||||

QY 241 LDAHRL 245  
|||||

DB 240 LDAHRL 244  
|||||

RESULT 15  
AAB26780  
ID AAB26780 standard; protein; 244 AA.  
XX  
AC AAB26780;  
XX  
DT 18-JAN-2001 (first entry)  
XX  
DE Human oestrogen receptor protein sequence.  
XX  
KW Homology model; ligand binding domain; glucocorticoid receptor; AIDS; hypertension; diabetes; obesity; glaucoma; depression; wound; human; protein co-ordinate data; thyroid hormone receptor; oestrogen receptor.  
KW  
OS Homo sapiens.  
XX  
PN WO200052050-A2.  
XX  
PD 08-SEP-2000.  
XX  
PF 01-MAR-2000; 2000WO-GB000727.  
XX  
PR 01-MAR-1999; 99GB-00004441.  
PR 22-APR-1999; 99GB-00009151.  
XX  
PA (KARO-) KARO BIO AB.  
XX  
PI Gillner M, Greenidge P;  
XX  
DR WPI; 2000-549565/50.  
XX  
PT Designing a homology model of the ligand binding domain of a glucocorticoid receptor displayed as a three-dimensional image, useful for identifying agonists and antagonists for treating e.g. inflammation, hypertension, glaucoma, diabetes.  
PT  
PS Disclosure; Fig 2A; 246pp; English.  
XX  
CC This invention relates to a method for designing an homology model of the ligand binding domain of a glucocorticoid receptor. The homology model may be displayed as a three-dimensional image. The method comprises: (a) providing an amino acid sequence and an x-ray crystallographic structure of the ligand binding domain of a thyroid, oestrogen or progesterone receptor; (b) modifying the x-ray crystallographic structure to take account of differences between the amino acid configuration of the ligand binding domain of the glucocorticoid receptor and the thyroid, oestrogen, or progesterone receptor; (c) verifying the accuracy of the homology model by comparing it with experimentally-determined binding properties of a number of ligands for the glucocorticoid receptor; and (d) modifying the homology model for greater consistency with the binding properties. The homology model is useful for drug screening and designing ligands (agonists and antagonists) capable of binding to a glucocorticoid receptor. The identified agonists are useful for the treatment of inflammation and also in immunosuppressive therapy. The identified antagonists are useful for the treatment of hypertension, diabetes, obesity, glaucoma, depression, acquired immune deficiency syndrome (AIDS) and wounds. The homology models are also useful for electronic screening of compound databases, de novo drug design and/or prediction of binding affinities of glucocorticoid receptor ligands for the receptor by

CC molecular mechanics scoring functions. The specification contains protein  
CC co-ordinate data for the glucocorticoid receptor models produced using  
CC the method, based on the X-ray crystallographic structure of the  
CC oestrogen and progesterone receptors. The present sequence represents the  
CC human oestrogen receptor protein. The protein is used in an example of  
CC the method of the invention for homology modelling based on the thyroid  
CC receptor  
XX  
SQ Sequence 244 AA;

Query Match 97.8%; Score 1202.5; DB 3; Length 244;  
Best Local Similarity 96.3%; Pref. No. 3e-134;  
Matches 236; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
QY 1 SLALSITADQVMSALLDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRV 60  
DB 1 SLALSITADQVMSALLDAEPPILYSEYDPTRPFSASMMGLLTNLADRELVHMINWAKRV 60  
QY 61 PGFVDLTLDQVHLLLECAWLEIMIGLVWRSMEHPGKLLFAPNLLLDNRNKGKCVGMEI 120  
DB 61 PGFVDLTLDQVHLLLECAWLEIMIGLVWRSMEHPGKLLFAPNLLLDNRNKGKCVGMEI 120  
QY 121 FDMLLATSSRFMRMNIQGEFVCLKSIILLNSGVYTFXXXXXXXKXKHHRVLDKIT 180  
DB 121 FDMLLATSSRFMRMNIQGEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 179  
QY 181 DTLIHLMKAGLTLOQOHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKVNVVPLYDILLEM 240  
DB 180 DTLIHLMKAGLTLOQOHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKVNVVPLYDILLEM 239  
QY 241 LDAHR 245  
DB 240 LDAHR 244

Search completed: November 8, 2004, 08:26:23  
Job time : 59.2408 secs